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THE UNIVERSITY OF ERISTOL

OS Phaseolus coccineus (scarlet runner bean)

PD 25-UTN-2002

PP 11-UTN-1999 UP 200554838

PR 12-UTN-1999 UP 200554838

PR 12-UTN-1999 UP 200554838

PR 12-UTN-1999 UP 200554838

PR 12-UTN-1998 UP 200554838

PR 12-UTN-1998 UP 200554838

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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
Phaseolus.
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/mol type="genomic DNA"
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AR452818
BT009225
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AB125233
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AR444996
AX008679
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AX008675
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   (bases 1 to 1318)
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JP 2002518005-A/1
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
BD243009
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AB181372 Vigna ang
CQ899251 Sequence
AV588429 Sequence
AV588978 Nerium ol
AV584229 Nerium ol
AV31563 Cucurbita
AJ302041 Cucurbita
AJ302041 Cucurbita
AJ302041 Cucurbita
AJ302041 Sequence
AR452811 Sequence
AR852817 Sequence
AB81373 Vigna ang
AR931206 Lactuca s
BT004464 Arabidops
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AR444991 Sequence
AX008671 Sequence
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                                                                                                                                                                                                                                  Description
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AB181372
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Gapop 10.0 , Gapext 1.0
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Minimum DB Maximum DB M

Database

Searched:

Sequence:

PAT 17-JUL-2003

linear

2

Result Š.

Db   1021 AGCTGATAATAGCCTCTTCCAGAAATCTGCTGATTAACCAAACACCCTT 1080	RESULT 2 AR444991 LOCUS DEPINITION Sequence 1 from patent US 6670527. ACCESSION AR44991 KEYWORDS SOURCE ORGANISM Unclassified. REFERENCE 1 (Dasses 1 to 1318) AUTHORS Thomas, S.G., Hedden, P. and Phillips, A.L. TITLE Gibberellin 2-oxidase JOURNAL Patent: US 6670527-A.I. THE UNIVERSITY OF Bristol; Bristol;	FEATURES 1.1318  Source 1.1318  Aorganism="unknown"  Mol_type="genomic DNA"  ORIGIN 100.0%; Score 1318; DB 6; Length 1318;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1318; Conservative 0; Mismatches 0; Indels 0; Gaps	Qy         1 GITTCTCTTCCTTACCCTGTTCTGCTTCTTTTTATAGTAACAATGGACAACAAC         60           bb         1 GITTCTCTTCCTTACCCTGTTCTGCTTCTTTTTCATAGTAACAATGGACAACAAC         60           Qy         61 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT         120           bb         61 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT         120	121 CAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAA  181 GAATCTCATAGTGAACGCTGTAGGGATTCCTGTGGTCTTCAAGCTTGTGAACCATGGCGA  181 GAATCTCATAGTGAACGCTGTAGGGATTCGGCTTCTTCAAGCTTGTGAACCATGGTGT  181 GAATCTCATAGTGAACGCTGTAGGGAACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT  241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAAATCTCA	
Best Local Similarity   100.0%;   Pred. No. 0;   Indels   0;   Gaps   0;   Matches   1318;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   Gaps	241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300 241 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300 241 TCCATTGGAGTTAATGGCCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300 301 GTCCGAGAAAGACTGGTCGCTCCCCCGACCCTTTCGGCTATGGTAGGAATGG 360 301 GTCCGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAAGAGATTGG 360 361 CCCAAACGGTGATGTCGGTTGGGTGGATACCTCCTCCACACACCAACGATTGTTAT 420 421 CTCACCCAAACGGTGATTTCCGAGAAAACCTCCTCATCATTTCAGGGGGGGG	481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTTTGGAATTGATGGTGGGGGG 540  481 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGTGGAGGG 540  541 GTTGGGGATAAGGCAGAGAATACGTTAAGCAGGTTGCTGAAGGATTGAAGAAAGTGATTC 600  541 GTTGGGGATAAGGCAGAAATACGTTAAGCAGGTTGCTGAAGGATGAAAAAGTGATTC 600  541 GTTGGGGATAAGGCAGAGAATACGTTAAGCAGGTTGCTGAAGGATGAAAAGTGATTC 600  601 GTGCTTCAGGTTGAACCACCCCGCTTAAGCAGAGGAAAGTGATTT 600	601 GGTTCAGGTTGAACCACTACCGGCTTGCCCTGAGGTGCAGCACCGGAATTT 660 661 GGTTGGGTTTGGGGAGCACACACACACACACATATTTCTGTCTTAAGATCTAACACGCAC 720 661 GGTTGGGTTTGGGAGCCACACACACACACAATAATTTCTGTCTTAAGATCTAACACACAC	TTCCTTTTCATCATGTGGTGACGTTACAGGTAATGACTAATGGGAGGTTTAAAAGTTCCTTTTCATTTTTCATTGGTGTGTGT	901 AGGACCAGCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATTAAAAGGAGAGA 960

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AX008671.1 GI:9996195 RESULT 3
AX008671
LOCUS
DBFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM

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. Phaseolus coccineus Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

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                                                                                                                                                                                                                                                                                    GTTTCTTCTTCCTTACCCTGTTCTGCTTCTCTTTTCATAGTAACAATCGACAACAACAAC
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                                                                                                                                                                                                                Score 1316.4;
Pred. No. 0;
                                                                                                                                                                                                                                                   0; Mismatches
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Best Local Similarity 99.9%;
Matches 1317; Conservative
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
Ashton Research Station, Long Ashton Research Station, Bristol,
BS41 9AF, UR
                                             TGTAAAGCATAGGGTTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGG
                                                                                                              AGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGATAAAAGGAGGAGGA
                                                                                                                                                               GTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCT
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                                                                                            AGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGGAA
                                                                                                                                                                                   GIGITICIACAAAAGACITCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCT
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Molecular cloning and functional expression of gibberellin oxidases, multifunctional enzymes involved in gibberellin deactivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLN
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Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2ox1
AJ132438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
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1. .1318
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/product="GA_2-oxidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3886"
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GA 2-oxidase, ga2oxl gene.
Phaseolus coccineus
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68. .1066
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Phillips, A.L.
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/product="gibberellin 2-oxidase"

/protein id="BAD99507.1"
/brotein id="BAD99507.1"
/db_xxef="di:67077912"
/db_xxef="di:67077912"
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Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete
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Submitted (08-JUN-2004) Masatoshi Nakajima, The University of Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan (E-mail:nkim@pgf1.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Gibberellin 2-oxidases from adzuki bean hypocotyl
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Brown, S.M., Elich, T.D., Heck, G.R., Kishore, G.M., Logusch, E.W.,
  ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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Gilbertson,L., Krieger,E., Zhang,W. and Ye,X.
Dna constructs and methods to enhance the production commercially viable transgenic plants
Patent: WO 200402330-A 3 28-OCT-2004;
Monsanto Technology LLC (US)
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/processin_id="AAT72916.1"
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Nerium oleander

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Gentianales; Apocynaceae; Apocynoideae;
Wrightieae; Nerium.

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Direct Submission
Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain
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Nerium oleander gibberellin 2 oxidase (GA2ox3) mRNA, complete cds.
AYS88978
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2 (bases 1 to 1406)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
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/mol_type="mRNA"
/db_xref="taxon:63479"
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Logusch, S.J., Piller, K.J., Rao, S., Ream, J.E. and Baerson, S.R. Methods for controlling glaberellin levels
Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, MO
Location/Qualifiers
                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                                            Length 1359
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                                                                                                                                                                                                                          Score 893.8; DB 6;
Pred. No. 5.3e-224;
1; Mismatches 158;
                                                                                                        1. .1359
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/wol_type="genomic DNA"
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Matches 1069, Conservative
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/ LTAIN 1 AL 10. ... MYVLSKPAMEQFCLVKNCKAPTLFPGVPLIDLSKPDSKHLLUKA
CQEFGFFKVINHGVPTEFITKLESEAVKFFSLPLSDKEKAGPPDPFGGNGKKIGPNGD
IGWYEXI ILSTNSEFNYQRFESI FGMTPEKFRDAVNDYVSSYKKAAGEI LELAMEGLN
IQPKNVFSKLLMDEQSDSYRLMHY PPYPDLQELHGRNLIGFGEHTDPQIISVLRSNN
TSGLQIQLKDGSWIS IPPDQSSFFINYGDSTQVLTNGRFKSVKHSNLSNN
YFGGPPLSEKIAPLPSLMEGEDSLYKEFTWFEYKKSAYKSRLADNRLVLFEKIAAS"
                                            PLN 30-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                         de Plantas, Consejo Superior de Biologia Molecular y Celular de Plantas, Consejo Superior de Investigaciones Cientificas (CSIC), Universidad Politecnica de Valencia, Avda. de los Naranjos s/n, Valencia 46022, Spain Location/Qualifiers
                                                                                                                                          Nerium oleander
Nerium oleander
Nerium oleander
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Gentianales; Apocynaceae; Apocynaideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCACATTATTCCCGGGTGTTCCATTGATAGACCTCTCGAAACCTGACTCGAAACACCTC 120
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1 (bases 1 to 1245)
Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Isolation, characterization and multi-site polyadenylation
20-oxidases and GA 2-oxidases in Nerium oleander
Unpublished
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Ubeda-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Ubrect Submission
Submitted (08-APR-2004) Instituto de Biologia Molecula
                                         1245 bp mRNA linear
2-oxidase 2 mRNA, complete cds
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larity 67.9%; Pred. No. 6.6e-111;
Conservative 0; Mismatches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Nerium oleander"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="GA 2-oxidase 2"
/protein_id="AAT92094.1"
/db_xref="GI:51011366"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:63479"
                                                                                                         GI:51011365
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                                                                                     ATTCAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGC
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                                              Gaps
  Length 1406;
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                                            Indels
  DB 15;
Score 484.6; DB 15;
Pred. No. 3.2e-116;
0; Mismatches 278;
Query Match
Best Local Similarity 70.4%;
Matches 677; Conservative
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GVPMELISSLESESTKFFSLPLSEKQRAGPPSPFGYGNKQIGRNGDVGWVEYLLLNTH
LESNSDGFISIFGQDPQKLSSAVNDYISAVRNMAGEILELMARGLKTQRNVFSKLVM
DEQSDSVFRVHYPPPCPDLALKGTWNIGFGEHTDPQIISVLRSNNTSGFQISLADGN
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PLASLMQGEERSLYKRFTWFEYKRSAVNSRLADNRLVPFERIAAS."
                                                                                                                                                                                            protein_id="CAC85924.1"
|db_xref="GI:32127337"
|translation="MAAASSFSAAFYSGIPLIDLSAPDAKQLIVKACBELGFFKVVKH
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                                                                                                                                     function="2-oxoglutarate dependent dioxygenase"
                                                                                                                                                                                                                                                                                                                                                                                        35.1%; Score 462.2; DB 15; Length 1383;
68.7%; Pred. No. 2.5e-110;
ive 0; Mismatches 293; Indels 3;
                                                                                                                                                       /codon_start=1
/product="Gibberellin 2-oxidase"
                tissue_type="root tips"
'dev stage="7 day old seedling"
[. .]383
    clone="2beta-WS2"
                                                                            /gene="ga2ox"
43. .1008
                                                                                                                 gene="ga2ox"
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Matches 651; Conservative
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Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
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Direct Submission
Direct Submission
Submitted (19-JUN-2001) Lange T., Botanical Institute, TU
Braunschweig, Mendelsschnstr. 4, D-38106 Braunschweig, GERMANY
related entry AJ315662.
Location/Qualifiers
CCACCGTTGAGTGAGATAGCTCCATTGCCATCACTTATG---GAAGGTGAAGACAGC
                                                          ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTTGATGGCGGAGGGGTTGGGG
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                                                                                                 GTATCATCAGTAAAGAAAATGGCTTGTGAAATACTTGAATTAATGGCAGAAGGTTTGAAT
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/mol_type="mRNA"
/culfivar="Riesenmelone, gelb/db_xref="taxon:3661"
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AJ315663.1 GI:32127336
Galos, gene, gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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A for gibberellin 2-oxidase 1, complete
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                                                                                                                                              CICATTGICAAAGCTIGIGAAGAACTCGGATICTTTAAGGTIGICAAACAIGGIGICCCC 227
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TCTGCAGCATTCTACTCTGGGATTCCATTGATAGACCTCTCTGCACCAGATGCTAAACAA
                                                                                                                                                                                                                   TIGGAGITAAIGGCCAATITAGAAAACGAGGCCCTCAGGTICITIAAAAAAICTCAGGTCC
                                                                                                                                                                                                                                                                                                                                                                     GAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                          288 gaaaaacagagagchggcccrrccrrrrrggcrarggaaacaaarrggccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 TCCTTCTTCATCAATGTTGGTGACTCTTTACAGGTGATGACTAATGGAAGATTCAAAAGT
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                                                                        CTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCA
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Nicotiana tabacum
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Nicotiana t
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/product="qibberellin 2-oxidase"
/product="qibberellin 2-oxidase"
/product="qibberellin 2-oxidase"
/product="qibberellin 2-oxidase"
/db_xref="dia-27123665"
/db_xref="dia-27123665"
/db_xref="coda-108GUD8"
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Direct Submission
Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Submitted (14-DEC-2000) Lange T., Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cucurbita maxima
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Cucurbitales, Cucurbitaceae, Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 TCCACGCCCTTGTTCACGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAAT 184
                                          843
                                                                                                               961
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GTGAAGCATAGGGTTTTGACAAACAGCTCGAAGTCAAGGGTTTCAATGATCTACTTCGGT
                                                                                                                                                                                        844 GGGCCACCGTTGAGTGAAAGATAGCTCCTTTAGCTTCCCTTATGCAAGGAGAAAGA
                                                                                                               GGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene) AJ302041. GI:27123664 ga2ox gene; gibberellin 2-oxidase. Cucurbita maxima (winter squash)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression studies on the major Gibberellin dioxygenases in developing seeds of Cucurbita maxima \boldsymbol{L}
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/function="2-oxoglutarate dependent gibberellin
dioxygenase"
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Pred. No. 1.7e-109;
0; Mismatches 295; Indels
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/dev stage="developing embryos"
1. .1308
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/mol_type="mRNA"
/cultivar="Riesenmelone, gell
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649; Conservative
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MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J.,
Gaskin, P., Lange, T. and Hedden, P.
Gibberellin biosynthesis from gibberellin Al2-aldehyde in endosperm
and embryos of Marah macrocarpus
Plant Physiol. 113 (4), 1369-1377 (1997)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I; Cucurbitales, Cucurbitaceae, Marah.
                                                                                                                                                      608 TGTTTTCAGGCTCAATCACTATCCCCCTTGTCCCGAGATTCAACAATTCAGTGACAATAA
                                                                                                                                                                                                                                           TTTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAG
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                                                        548 ATTAAATATTCATCCTAGGAACGTTTTCAGTAAACTTCTAATGGACGAAAAGAGTGACTC
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CbefgffkvjnhsvptbfjtklbsbajkffssplsekQkagpadpfgnkkjgpngd
Vgwybytllstnsbfnsefnyhkfasilgvnbetjibanddyvskkkagetilbmlabglid
HPRNVFSKLLMDEKSDSVPRLMHYPPCPEIQQFSDNLJGFGHTDPQ1ISVLRSN
TSGLQILLKNGHNJRYPPCPPIQQFSDNLJGFGHTDPQ1ISVLRSN
TSGLQILLKNGHNJRYPPCPPIQVRJNTNGFRKSVTHRVLANSVKSRLSNI
YFGGPPLSEKIAPLASLMBGESLYEBFTWFBYKKSAYKTRLADNRLVLFEKVAAS"
                                                                                                                                                                                                                                 Sakane, M., Nakajima, M. and Yamaguchi, I.
Direct Submission
Submitted (28-0013) Masayuki Sakane, University of Tokyo,
Applied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo,
113-0032, Japan (E-mail:m-sakane@pgrl.ch.a.u-tokyo.ac.jp,
URL:http://pgrl.ch.a.u-tokyo.ac.jp/, Tel:81-3-5841-5158(ex.25158),
Fax:81-3-5841-8025)
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Pred. No. 6.6e-108;
0; Mismatches 355; Indels
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/protein_id="BAD17855.1"
                                                                                                    Molecular cloning of GA 2-oxidase in BY-2 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Nicotiana tabacum"
/mol_type="mRNA"
/db_xref="taxon:4097"
/cell_line="BY-2"
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(bases 1 to 1352)

Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr., Allen,S.M., Kinney,A.J., Lee,J.-M., Lohman,K.N., Rendina,A.R., Sakai,H., Famodu,O.O., Lee,J.-M., Lohman,K.N., Rendina,A.R., Sakai,H., Weng,Z., Caimi,P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L., Sakai,H., Weng,Z., Caimi,P.G., Helentjaris,T.G. and Li,C.P. Plant metabolism genes

Plant metabolism genes

Patent: US 6677502-A 13 13-JAN-2004;

E.I. du Pont de Nemours and Company and Pioneer Hi-Bred

International; Wilmington, DE

Location/Qualifiers

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                                                                                   GGAGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAG
                                                                                                                                    1029 agaaagirirgiacaaagagiricacrirggirigagiacaagaagaacagcriacaag
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US 6677502.
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CTTCAAGCTTGTGAACCA

354 452 414 512 474

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TGGTGTCTCCATGGAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTCTAT
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                                                                   TGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA
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Allen,S.M., Kinney,A.J., Rafalski,J.A., Orozco,E.M. Jr.,
Miao,G.-H., Famodu,O.O., Lee,J.-M., Lohman,K.N., Rendina,A.R.,
Sakai,H., Weng,Z., Caimi,P.G., Fang,Y., Shen,J.B.J., Zoughi,I.L.,
Anderson,S.L., Shi,J., Lu,G., Helentjaris,T.G. and Li,C.P.
Plant metabolism genes
Patent: 108 6677502-A 5 13-JAN-2004;
B.I. du Pont de Nemours and Company and Pioneer Hi-Bred
International; Wilmington, DE
Location/Qualifiers
                                                                    914 CCGAAGTGTGAGACACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTA
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                                                       TGATICGIGCTICAGGITGAACCACIACCGCCTIGCCCTGAGGIGCAAGCACTGAACCG
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GGAGGGGTTGGGGATAAGGCAGAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAG
                          614 agaaggerrgaagarrcagcaaaaggargrerrragcaagcrrcraarggaraacaaag
                                                                                                             GAATTTGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAA
                                                                                                                                                                   CAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGA
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Sequence 5 from patent US 6677502.
AR452817

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981 CTTTGGAGGTCCACCTTTGAGTGAGAAAATAGCACCATTATCCTCTCATG---AAAGG 1037
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                                              861 TGACAAATCCTTTTTTTATTAACGTTGGTGATTCTCTTCAGGTTATGACAAATGGAAGGTT
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Adm94201 Rice Diox Adm94201 Corn Diox Add9264 Cotton gi Add16264 Cotton gi Add15210 Rice isop Adx13286 Plant ful Adx09682 Plant ful Adx09682 Plant ful Adx69812 Rice gene Adx6986 Plant ful Adx60268 Maize gib Add68659 Arabidops Add10265 Cotton gi Add10265 Arabidops Adc50271 Arabidops Adc50271 Arabidops Aac59377 Arabidops Aac59377 Maize gib Add10267 Maize gib

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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SO.	Description	Aaz55912 Runner be	Adt62692 DNA encod	Aaz99471 Soybean g	Aad40261 Soybean G	Adm94213 Soybean D	Adm94205 Soybean D	Aaz55916 Arabidops	Abz13545 Arabidops	Ada67975 Arabidops	Aaz99472 Soybean g	Aad40262 Soybean G	Aaz55917 Arabidops	Adm94207 Wheat Dio	Aac39277 Arabidops	Aaz55915 Arabidops	Aeb67733 Rice geno	Ada70120 Rice gene	Adk00081 Rice CDNA	Aeb67784 Rice geno
SUMMAKIES	ΩI	AAZ55912	ADT62692	AAZ99471	AAD40261	ADM94213	ADM94205	AAZ55916	ABZ13545	ADA67975	AAZ99472	AAD40262	AAZ55917	ADM94207	AAC39277	AAZ55915	AEB67733	ADA70120	ADK00081	AEB67784
	DB	m	13	m	9	12	12	m	9	60	٣	9	٣	12	٣	m	14	æ	17	14
	* Query Match Length DB	1318	666	1359	1359	1352	1365	1237	1026	1026	1403	1403	1008	1473	1224	1316	1651	984	984	1271
	% Query Match	100.0	75.8	67.8	67.8	32.7	32.6	32.3	32.3	32.3	32.2	32.2	29.0	27.6	27.1	27.1	27.0	26.9	26.9	26.9
	Score	1318	666	893.8	893.8	430.8	429.2	425.8	425.4	425.4	424.8	424.8	382.8	363.6	356.6	356.6	355.6	354	354	354
	Result No.		7	٣	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19

AAZ55912 standard; cDNA; 1318 BP. AAZ55912;
(first entry)
Runner bean gibberellin 2-oxidase PcGA2ox1 cDNA.
Gibberellin 2-oxidase, PcGA2ox1; runner bean; 2-beta-hydroxylation; inactivation; growth inhibition; ss.
Phaseolus coccineus.
Location/Qualifiers
/*tag=
99WO-GB001857.
98GB-00012821. 98GB-00015404.
(UYBR-) UNIV BRISTOL.
Hedden P, Phillips AL;
WPI; 2000-097742/08. P-PSDB; AAYS8597.
New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
Claim 1; Fig 1; 42pp; English.
Key CDS MO9966029-A2. 23-DEC-1999. 11-JUN-1999; 15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 15-JUL-1998; 16-JUN-1998; 16-JUN-1999; 16-JUN-19

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40 40 00 8 60 9

80

This sequence represents cDNA encoding a runner bean gibberellin (GA) 2cxidase, PcGAZOXI. This enzyme is a GA 2-beta-hydroxylase that acts on
CC Oxidase, PcGAZOXI. This enzyme is a GA 2-beta-hydroxylation is to control of a GA results in a biologically
CC Hydroxylation at the 2-beta-hydroxylation of a GX results in a biologically
inactive product, and is the most important route for GA metabolism in
CC plants, ensuring that the active hormones do not accumulate in plant
CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
CC enhanced to reduce the concentration of bioactive GAs in the plants and
C therefore to inhibit plant growth of social crown such as enhancing lodgingCC resistence and grain yield in cereals, improving seedling quality,
C reducing the growth of amenity grasses, reducing shoot growth in orchard
and ornamental trees, improving tolerance to cold, drought and infection,
CC and increasing yields (by the diversion of assimilates from vegetative to
Creproductive organs). The nucleic acids may also be used to induce male
and/or female sterility (by expression in floral organs), prevent preCC fearus sprouting, reduce shoot growth in hedging plants, inhibit
C reversibility in the development or gerwination of seeds and reduce shoot
CC growth in commercial wood species. Antisense constructs of the nucleic
CC acids can also be used to transform plants to reduce the expression of GA
C 2-oxidase (Claimed) to promote plant growth, (e.g., to improve fruit set
CC and growth in seedless grasse, citrus fruits and pears), improve skin
CC texture and fruit shape in apples, increase stem length and rherefore
C increase growth in woody species
CC improve malting yields and quality in cereals (particularly parley), and
CC improve malting yields and darality in cereals iparticularly barley), and
CC improve organs.

Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

300 420 61 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT 120 180 CAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAA 180 240 240 TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCA 300 GTCCGAGAAAGACAGAGCTGGTCCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGG 360 Grcceaeaaacacaedcrecrececedacerrrececrarecraecaacaedearrec 360 CCCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCAACACACCAACCCTGATGTTAT 420 480 CTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGA 480 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGG 540 GAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGG 540 GTTGGGGATAAGGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC 600 61 AACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATT 120 GTTTCTTTCTTACCTTACCCTGTTCTGCTTCTTTTTCATAGTAACAATGGACAACAACAAC 60 CAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAA GAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT TCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAAATCTCA GTTTCTCTTCCTTACCCTGTTCTGCTTCTTTTTTCATAGTAACAATCGACAACAAC GAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGT CTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGGGGGTGGT Gaps ; DB 3; Length 1318; 0; Indels Query Match 100.0%; Score 1318; Best Local Similarity 100.0%; Pred. No. 0; Matches 1318; Conservative 0; Mismatches 121 361 121 181 241 241 181 301 301 361 421 481 481 541 421 셤 ò g ઠે 셤 õ g ઠે 셤 8 ò a ò ద ò 유

GTGATTC 6								ACCCTT 1	TTTTCC 1        TTTTCC 1	ATAGGT 1	CAACTT 1	AAAA 131      AAAA 131	nsgene;
rgagaaaa(	ACTGAACCO	AAGATCTAA	CCACCTG	rgggaggtj 	AATGATCTZ	STTAAAAGC	STACACTTO             STACACTTO	ACCAAACA(	CCTTTTT 	AGAAAATGI            AGAAAATGI	AGTTGGTCT             AGTTGGTCT	48888888888888888888888888888888888888	Bmid; tra
CTGAAGGA	GTGCAAGC           GTGCAAGC	TCTGTCTT.	GTTTCAGT	ATGACTAA          ATGACTAA	AGGTTATC	TCAGTGAT         TCAGTGAT	AAGGCTGO          AAGGCTGO	GCTGATTA          GCTGATTA	ATTTTCTT             ATTTTCTT	ACATATAT.          ACATATAT.	AGTGTAAC          AGTGTAAC	acaaaaa         acaaaaaa	2-oxidase um Ti pla enic; pla
GCAGGTTG	CTTCAGGTTGAACCACTACCGGCCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTT 	GGTTGGGTTTGGGGAGCACACACACACAGATAATTTCTGTCTTAAGATCTAACAGCACACACA	ATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGAC 	TTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGGTTAAAAG 	TGTBABGCATBGGGTTTTGGCTGBCCBAGGTCBAGGTTATCBATGATCTACTTTGG 	aggaccagcgttgagtgaaaatatagcacctttaccttcagtgatgttaaaaggagagga 	GTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCT 	agctgataataggcttgcccctttccagaaatctgctgctgattaaccaaacacgcctt 	CAARTICCACTCATTITACGCACGTGTTATTACCCCAATTITCTTTCCTTTTTCTTTTC	TGTGTCTGTCTAGGTTTCAAACAGTTGACTCTACTTGACATATATAGAAAATGAATIAGGT 	TAAGATGTTTATCATTTTCTTGTTTCATCTAAGTGTAACAGTTGGTCTCAACTT 	CTTTCCTCAATTGTCAATGGAACGCAACTCTAGTTACAAAAAAAA	erellin 2 obacteriu , transge
TACGTTAA	CCCGCCTT 	AGACCCAC	CACAGATG	TGACGCTC	TGACACAA          TGACACAA	TATAGCAC          TATAGCAC	ATGGTGTG          ATGGTGTG	TTTCCAGA          TTTCCAGA	ACGTGTTA          ACGTGTTA	CAGTTGAC           CAGTTGAC	TTTCTTGT          TTTCTTGT	GAACGCAA          GAACGCAA	P. eus gibbe DNA, Agro ic plant;
GGCAGAGGAA	AACCACTA	GAGCACAC	ATCTGTCT 	AATGTTGG		agtgaaaa          agtgaaaa	GAGTTCAC           GAGTTCAC	CTTGCCCC	TTTTACGC           TTTTACGC	GTTTCAAA           GTTTCAAA	ATTTTCTT          ATTTTCTT	TGTCAATG	ttry) it coccine coccine number T-D number T-D d d s.
GGGGATAAGG	TCAGGTTG          TCAGGTTG	GGTTTGG 	GCTTGCAP          GCTTGCAP	TTTTCATO	AGCATAGO	CAGCGTTG	TGTACAAA          TGTACAAA	ataatagg          ataatagg	TCCACTCA          TCCACTCA	CTGTCTAG           CTGTCTAG	TGTTTATC           TGTTTATC	rccrcaai          rccrcaai	162692 standard; DNA; 999 162692; JAN-2005 (first entry) A encoding Phaseolus cocci A plasmid; transfer DNA; Tression cassette; transgroberellin 2-oxidase; ds. 18004092390-A2.
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The present invention relates to a DNA plasmid comprising a transfer DNA (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked to at least one transgene linked to an Agrobacterium Ti plasmid second corder region, and located in the DNA plasmid outside of the T-DNA is a plant expression cassette comprising a plant cell non-lethal negative selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgenie in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal comparities the linked non-lethal negative selection marker gene. The promoter expresses the linked non-lethal negative selection marker gene. The promoter expresses the linked non-lethal negative selection marker gene comprises a plant hormone biosynthetic pathway gene, degradative gene, biosynthetic pathway can degradative selectable marker gene comprises a plant hormone comprises a transgene of signalling gene, or metabolic interference from antibiotic resistance and herbicide resistance. The transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway gene is selected from gibberelit acid pathway.
                                                                                                                                                                                                       New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid first border region linked to a transgene linked to an Agrobacterium Ti plasmid second border region, useful for enhancing production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway genes, and abscialc acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence represents DNA encoding Phaseolus coccineus gibberellin
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09-APR-2003; 2003US-0461459P.
                                                    (MONS ) MONSANTO TECHNOLOGY
                                                                                                        Krieger E,
                                                                                                                                                         WPI; 2004-758349/74.
                                                                                                                                                                                                                                                                                            transgenic plants.
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Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

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                                                     ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTTCTGAAACCATTCAAGTCC
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128 AAAICACTITIGCATITICCGAGAAAATCCICATCATITICAGGGCGGTGGTGGAGAACTAC
                                                                          TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
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                                                        188 ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG
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/product= "GA 2-oxidase 1 protein"
/transl_except= (pos:633. .635, aa:Xaa)
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                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a gibberellic acid 2-oxidase 1 protein describes which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels and interest or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-xidase, phytones synthase, C-20 oxidase, and a 2beta-hydroxylase polynucleotides to achieve this. The method is used to control seed gibberellin biosynthetic pathway and restoration of normal seed gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
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Pred. No. 3.5e-237;
1; Mismatches 158; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                                                   Kishore GM, Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                     Claim 45; Page 248; 267pp; English
                                                                                                                                                 Heck GR,
99WO-US018066
                                        98US-0096111P
99US-0137977P
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Best Local Similarity 84.9%;
Matches 1069; Conservative
                                                                                                                                                                       Rao S, Ream JE;
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                                                                                                      (MONS ) MONSANTO CO
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P-PSDB; AAY84099.
10-AUG-1999;
                                        10-AUG-1998;
07-JUN-1999;
                                                                                                                                               Brown SM,
Piller KJ,
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                                                             519 TACATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGAGGGATTG
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The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in garicultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA-oxidase 1 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
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67.8%; Score 893.8; DB 6; Length 1359;
Best Local Similarity 84.9%; Pred. No. 3.5e-237;
Matches 1069; Conservative 1; Mismatches 158; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                    Logusch EW,
  amino acid"
                                                                                                                                                                                                                                                                  Kishore GM,
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/note= "Xaa = any
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completed sequence encoding a polypeptide having GTP cyclohydrolase in 1/3,4-dihydrovy-2-butanone-4-phosphate synthase activity, appearing as DM94266. Also included are a recomprising the polymucleotide operably linked control and a sequence encoding a plant comprising the polymucleotide operably linked control and construct comprising transforming a cell with the polymucleotide, a cell comprising transforming a cell with the polymucleotide and regenerating a plant from the transformed plant cell), a plant comprising transformed a plant cell with the polymucleotide and regenerating a plant from the transformed plant cell), a plant comprising the recombinant DNA construct. Also disclosed as new are mucleic acid (CDNA) fragments and assembled contigs encoding plant metabolism proteins consen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate companies. Dioxygentase, Ribcflavin specific deaminase, Ethylane response consent from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate companies. Dioxygentase, Ribcflavin specific deaminase, Ethylane response consent from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate companies. Dioxygentes in Peglycoprotein I, Peglycoprotein I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to an isolated polynucleotide comprising a
ABC transporter GCN20-like, P-glycoprotein I; P-glycoprotein 3; P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter; PMP70 ABC transporter; MRP4 ABC transporter; transgenic.
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                                                                                                                                                                                                                                                                                           146 AACAACAAGAAAATGGTGTTGTTGTCCAAAGCAACAGAACAGAATACTCCTACATTAA
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                                                                    Score 430.8; DB 12; Length 1352;
Pred. No. 1.2e-108;
0; Mismatches 332; Indels 15;
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Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;
                                                                    32.7%;
al Similarity 65.7%;
665; Conservative (
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nucleotide sequence encoding a polygeptide having GTP cyclohydrolase

II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as

ECC II/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as

ECC ADM94266. Also included are a vector comprising the polynucleotide, a

recombinant DNA construct comprising the polynucleotide operably linked

to at least one regulatory sequence, transforming a cell with the

ECC to at least one regulatory sequence, transforming a cell with the

ECC producing a plant (comprising transforming a plant cell with the

ECC polynucleotide and regenerating a plant from the transformed plant cell),

ECC a plant comprising the recombinant DNA construct and a seed comprising

the recombinant DNA construct. Also disclosed as new are nucleic acid

(CDNA) fragments and assembled contigs encoding plant metabolism proteins

CCDNA) fragments and assembled contigs encoding plant metabolism proteins

CCDNA) fragments and assembled contigs encoding plant metabolism proteins

CCDNA) fragments and assembled contigs encoding plant metabolism proteins

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CCDNA) fragments and assembled contigs encoding plant metabolism proteins

CCDNA) fragments and assembled contigs encoding plant metabolism protein

CCDNA) fragments and assembled contigs encoding plants, P-glycoprotein ATPOP, P-glycoprotein

CCDNA) fragments are present at higher or lower levels than normal or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famoαu CO;
, Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
JB, Zoughi IL, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                      Soybean; ss; plant; plant metabolism; GTP cyclohydrolase II/3, 4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenaes; Ent-Kaurene Synthase A; GA-20 oxidase; Gdibberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; P-glycoproter GTOX20-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein APPGP; P-glycoprotein HVMDR2; AGC transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to an isolated polynucleotide comprising a
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                        ADM94205 standard; cDNA; 1365 BP
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99US-0146650P.
99US-0170906P.
99US-0172946P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUL-2000; 2000US-00614912
                                                                                                                                                      Soybean Dioxygenase cDNA #1
                                                                                                            (first entry)
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P-PSDB; ADM94206.
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21-DEC-1999;
21-DEC-1999;
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Lee J,
Shen JB,
                                                                 ADM94205;
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cell types or in developmental stages in which they are not normally found. The polynucleotides can be used as probes for genetically and physically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length colymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes consisting the mutation products generated from the mutation population using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypoptides in altu in cells or in vitro in cell extracts. The present sequence encodes a plant metabolism protein (or \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

~ 212 234 TGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA 294 354 452 414 512 474 560 174 295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAG TGCCAAGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCA 33 TGGTGTCTCCATGGAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTTAT 153 AACAACAAGAAAATGGTGTTGTTGTCCAAAGCAACAACAAGAACAATACTCCTACATTAA 393 grcacrcaargaaaagaaaaagraagaccrcccaarccarraggrarggragcaagaa 453 AATTGGACACAATAGGGACGTTGGTTGGATTGAGTACCTTCTTCTCAACACACCAATCAAGA 55 AACAACAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAA 115 ACCATTCAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGA 213 gaacigcargccaaccaaarirriccicaacaarircccaragiggaccrcraaacciga 35 GATTGGCCCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCAACCCTGA 415 TGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGT Gaps Score 429.2; DB 12; Length 1365; Pred. No. 3.3e-108; 0; Mismatches 333; Indels 15; cal Similarity 65.6%; 664; Conservative 32.6%; 273 175 235 Query Match Best Local Matches 66 셤 셤 유 g 임 à g ð Š ò ઠે ò ઠે

620 513 ACACAACT------TCTCTGTTTATGGCAAAACCCTGAGAATTCAGGTGTCT GGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGC 475

681 741 655 셤 Š g

740 594 621 AGAAGGGTTGAAGATTCAGCAAAAGGATGTTTAGCAAGCTTCTAATGGATAAACAAAG 680 654 714 800 774 561 GTTGAACAGTTACATGTCTTCTGTGAGGAAGATGGCATGTGAGATTCTTGAGTTGATGGC TGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAACCG GAACTIGATIGGGTITIGGGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAA CAGCACATCTGGCTTGCCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGA CAACACTICAGGCCTICAGATITATCTIAGAGATGGAAATTGGATTTCAGTCCCACCAGA GGAGGGGTTGGGGATAAGGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAG reactionariticases da arcaniación esta constructo de arcana de arca 595 715 쉱 ઠે 셤 ò 엄 ò ò

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                                                                                                                       AGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTAAATACAAGAAGGCTGCGTACACTTC 1014
                                                                                                                                              This sequence represents CDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PcGA2ox2. This enzyme is a GA 2-beta-hydroxylation at Let and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant issues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling
                        894
                                                                       954
861 TGACAAATCCTTTTTTATTAACGTTGGTGATTCTCTTCAGGTTATGACAAATGGAAGGTT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                               921 CCGAAGTGTGAGACACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTTA
                       835 TAAAAGTGTAAAGCATAGGGTTTTGGCTGACAAAGGAAGTCAAGGTTATCAATGATCTA
                                                                       CTTTGGAGGACCAGCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGG
                                                                                                                                                                                                                                                                                                                                                           2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                      1015 AAGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
                                                                                                                                                                                             1098 AAGATTATCTAAAAATAGACTTGAACATTTGAAAGAATTGCAGCTTCGTAA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Gibberellin 2-oxidase AtGA2ox2"
                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                           AAZ55916 standard; cDNA; 1237 BP
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98GB-00015404
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                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
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quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), prevent pre-harvest sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and learn), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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                                                                                                                                                           GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGGCTGAC 865
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GACTICGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTA
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                                                                          TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
                                                                                                          1036 TCTCAATACAAATCTTCTGCTTACAAGTCTAAGCTTGGTGATTATAGACTTGGTCTCTTT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell production of transgenic plants. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ1754) used not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
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                                            976 GCACCATTGCCATGCCTTGTCCCTGAGCAAGATGATTGGCTTTACAAAGAATTCACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a stress condition to which a plant cell has been exposed producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                          CAGAAATCTGCTGCTGATTAACCAAACACCCCTTCAAATTCCACTCAT 1094
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Pred. No. 3.3e-107;
0; Mismatches 306; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana stress regulated gene SEQ ID NO 1350.
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana; plant; gene; stress; transgenic;
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                    GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGGCTGAC 865
                                                                                                                                                                                                                                                                    ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obtaining transgenic plant useful for controlling seed germination and
                                                                                   GCTCTTCAGGTTATGACTAACGGGAGGTTCAAGAGTGTTAAACACAGGGTCTTAGCCGGT
                                                                                                                                                                                                                                                                                              ACAAGGAGATCGAGGATTTCAATGATATTTTCGGCGGGCCGCCATTGACCCGGAAGATC
CCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTTGGGTTTTGGGAGCACACAGAC
                             GC---GGCGGAGGAAGACGCGGAGAAGATGGTGAAGGTGGGGTTTGGGGAACACACAGAC
                                                                 CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
                                                                                                                                   GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGAC
                                                                                                                                                                   GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                                                                                                   GCACCATTGCCATGCCTTGTCCCTGAGCAAGATGGTTGGCTTTACAAAGAATTCACTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Logusch
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99US-0137977P.
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Ream JE;
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07-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625
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                                                                                                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGCÁGGAGGCTATTGGCTTCGCCTTGCCTCAGTCTCTTAAAAACCGGGCCGGTCCA
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                                                                                                                                                                                                    Hou Y;
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Zhu
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                                                                                                                                                                                                  Glazebrook J, G
Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                     Claim 6; SEQ ID NO 223; 899pp; English.
                                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                 22-JUN-2001; 2001WO-IB001105
                                                                                                                                  22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                                   Tao
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Arabidopsis thaliana
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622; Conser
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                             WO2003000898-A1
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Matches 622,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
                                                                      GATCACAAAATCTTTCATAAATGTTGGTGAATTCTCTTCAGGTTATGACCAATGGAAGG
                                                                                                                                 TITAAAAGTGTAAAAGCATAGGGTTTTTGGCTGACAACGAAGTCAAGGTTATCAATGATC
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                                               GATCAGACTTCCTTTTTCATCTTGGTGACGCTCTACAGGTAATGACTAATGGGAGG
779 AACAATACTTCAGGCCTTCAGATTTTTCTTAGAGATGGAAACTGGATTTCAGTCCCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                     1076 TCAAGATTGGCTGATAATAGGCTTGGACATTTTGAGAGAATTGTTGCTTCATAA 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberellin, transgenic plant, seed germination, seedling growth; transgenic, 2-oxidase 2, enzyme, GA, soybean; gene, ss.
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/product= "GA 2-oxidase 2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 45; Page 94-95; 155pp; English.
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149. .1129
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                                                                                                       The present sequence encodes a gibberellic acid 2-oxidase 2 protein sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                532
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    seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 424.8; DB 3; Length 1403; Pred. No. 5.6e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 327;
                                                                      Claim 45; Page 250; 267pp; English.
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66.0%;
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Matches 669; Conservative
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normally reducing agronomic output can be avoided and yields increased. Plants a slso demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
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al Similarity 66.0%;
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This sequence represents cDNA encoding an Arabidopsis thaliana gibberallin (GA) 2-oxidase, PcGA20x3. This enzyme is a GA 2-beta-gibberallin (GA) 2-oxidase, PcGA20x3. This enzyme is a GA 2-beta-cc gibberallin (GA) 2-oxidase, nc 19-6As and for which 2-beta-hydroxylation is is is conly activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant tissues. The nucleic acids can be used to transform plants so that gibberallin 2-oxidase can be constitutively over-expressed or or otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and hortcultural applications such as enhancing or ordered and ornamental trees, improving yrasses, reducing shoot growth in ordered and ornamental trees, improving tolerance to cold, drought and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to indibit reversibility in the development or gerowth in hedging plants, chibbit reversibility in the development or gerowth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the
                                   1075
GGAGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth
                     1013 TCAAGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGATTAA 1066
                                                                                                1076 TCAAGATTGGCTGATAATAGGCTTGGACATTTTGAGAGAATTGTTGCTTCATAA 1129
                                                                                                                                                                                                                                                                                                                                                          Gibberellin 2-oxidase; AtGA2ox3; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Gibberellin 2-oxidase AtGA2ox3"
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1008
/*tag= a
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                                                                                                                                                                                                       AAZSS917 standard; DNA; 1008 BP
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                                                                                                                                                                                                                                                                                10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas SG,
953
                                                                                                                                                                                                                                             AAZ55917;
                                                                                                                                                                    RESULT 12
AAZSS917
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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield is sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 382.8; DB 3; Length 1008; Pred. No. 2.2e-95;
                                                                                                                                                                                                                                                                                                                    Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 327; Indels
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nes 595; Conservative
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New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Orozco EM, Miao G, Famodu OO;
ai H, Weng Z, Caimi PG, Fang Y;
Shi J, Lu G, Helentjaris TG;
                                                                                                                                                        Wheat, ss; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; PaGC transporter GGN20-like; Peglycoprotein I; Peglycoprotein 3; Peglycoprotein ATPGF; Peglycoprotein HVWMR2; ACC transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rendina AR, Sakai H, Weng Z,
Anderson SL, Shi J, Lu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; SEQ ID NO 7; 186pp; English.
1046 CAGAAATCTGCTGCTGATTAACCAAACA
                 973 gagaacciccarrircrcrarcca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rafalski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                         99US-0143401P.
99US-0143412P.
99US-0146650P.
99US-0170906P.
                                                                        ADM94207 standard; cDNA; 1473
                                                                                                                                                                                                                                                                                                                      2000US-00614912
                                                                                                                                                                                                                                                                                                                                                                                               99US-0172959P
                                                                                                                 (first entry)
                                                                                                                                     Wheat Dioxygenase cDNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lohman KN, Re
Zoughi IL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-088430/09.
P-PSDB; ADM94208.
                                                                                                                                                                                                                                                        Triticum aestivum.
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                                                                                                                 17-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                     21-DEC-1999;
21-DEC-1999;
                                                                                                                                                                                                                                                                                                  13-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee J, Lo
Shen JB,
Li CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allen SM,
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                                                             ADM9420
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HVMDR2, ABC transporter, PMP70 ABC transporter and MRP4 ABC transporter.

The nucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally cell types or in developmental stages in which they are not normally bysically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as probes for genetically and polymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation probes against the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or protecins comprising the amino acid sequences. Antibodies are useful for extracted.

The present sequence encodes a plant metabolism protein (or extracted).
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Sequence 1473 BP; 285 A; 440 C; 468 G; 280 T; 0 U; 0 Other;

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299 419 479 539 649 709 779 CAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCAT 119 120 TCAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCA 179 239 298 359 AGGCCGACAAGGACCGCTCCGGCCCGGCCTACCCGTTCGGCTACGGCAAGCGCATCG 418 TCTCCGGCGCCTGCCCGTCCCGTCCTGCG------CGCTCTTCCGGGCGGCGCTGA 529 589 GGTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATT 599 CGTCCGGCCTGCAGATCGCGCTCCAGAACGGGCAGTGGGTGTCCGTGCCCTCGGACCGCG 829 CAGCCATGGTGGTTCTCGCCAGCACGCCGCCGTCGATCACATCCCGCTCCTCAGGTCGC 178 238 AGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTG TTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAATCTC <u> AGTCCGAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTG</u> GCCCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGATGTTA GGCTCAATGGCGACATGGGGTGGCTCGAGTACCTGCTCCTGGCCGTCGACTCCGCGTCGC TCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGG <u> AGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGG</u> <u> accaderaciar ceceses de casas de casa</u> CGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAACCGGAATT 660 TGGTTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCA 710 CCACCGGCTTCGGCGAGCACGGACCCGCAGCTCATCTCCGTGCTGCGCTCCAACGGCA CATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGA GGCTGGGCATTGCGGCCGTGGACGCGCTGAGCGGGATGGTGACGGCGGAGGGGAGCGACC Gaps Length 1473; 9. 0; Mismatches 374; Indels Score 363.6; DB 12; Pred. No. 5.6e-90; cch al Similarity 61.3%; 607; Conservative Best Local Similarity 179 180 540 09 419 480 530 290 009 650 770 119 239 240 299 300 359 360 420 479 Match Matches 유 8 g g ð g 유 a a 셤 g ð ð ò ઠ ò ઠે ò 셤 õ 8 δ

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                                                                                                                                                                                                                                                                                                         Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
780 CTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAA
                                                                            900 GAGGACCAGCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGG
                                                                                                                                     GTGTAAAGCATAGGGTTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTG
                                                        GCGTGAAGCACAGGGTGGTGGCCAACAGCCTAAAGTCTAGGGTTTTCCATGATCTACTTTG
                                                                                                                    960 AGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGC
                830 aceccricricercaacercesceacricerrecaeserecreaceaeseserreaga
                                                                                                                                                                                                                                                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 24035.
                                                                                                                                                           1020 TAGCTGATAATAGGCTTGCCCCTTTCCAGA 1049
                                                                                                                                                                              1070 regegeacaacaecreecreacriceaca 1099
                                                                                                                                                                                                                                ВÞ
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99US-0123548P.
99US-0125248P.
99US-0126264P.
99US-01267462P.
99US-0128734P.
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99US-013843P.
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99US-0132863P.
99US-0134218P.
99US-0134219P.
99US-013421P.
99US-013430P.
99US-0134768P.
                                                                                                                                                                                                                               AAC39277 standard; DNA; 1224
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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30-APR-1999;
30-APR-1999;
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05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                     17-0CT-2000
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19-MAY-1999;
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08-APR-1
16-APR-1
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			13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999;
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AAZ55915 standard; cDNA; 1316
                                                   RESULT 15
                                                                           AAZ55915
                                                                                                      GTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAG 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722
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                                                                                                                                                                                                                                                                                                             CCGGGTTCTCTCTAATCCCGGTTATAGATATGTCTGACCCAGAATCCAAACATGCCCTCG 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 CCCAAGTCG---CAGGTTATCCCTTAGGATACGGGAACAGTAAGATTGGTCGGAATGGTG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTCGGTTGGGTCGAATACCTCCTCCAACACCCAACCTGATGTTATCTCACCCAAAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGTGGGTTGGGTTGAGTACTTGTTGATGAACGCTAATCTTGATTCCGGTTCGGGTCCAC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTTTGCATTTTCCGAGAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTACATTA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           552 GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGT
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                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                         12;
                                                                                                                                                      Length 1224;
                                                                                                                                                                                                         Indels
                                                                                                                                                         DB 3;
                                                                                                                                                                                 Pred. No. 4.5e-88;
0; Mismatches 329;
                                                                                                                                                         Score 356.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGATAATAGGCTTGCCCCTTTCCAGA 1049
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99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
                                                                                                                                                    Query Match 27.1%;
Best Local Similarity 63.2%;
Matches 586; Conservative
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PcGA2ox1. This enzyme is a GA 2-beta gibberellin (GA) 2-oxidase, PcGA2ox1. This enzyme is a GA 2-beta cut of the product of the conflict on C19-CAS and for which 2-beta bydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not accumulate in plant tissues. The nocleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed or otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing in many agricultural and horticultural applications such as enhancing calling realists and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance to cold, drought and corbard and ornamental trees, improving tolerance or assimilates from vegetative to reproductive organs). The nucleic acids may also be used to inhibit reversibility in the development or germination of seeds and commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids, used
                                                                                                                                                                                                                                                           2-oxidase; AtGA2ox1; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed plant gibberellin 2-oxidase enzymes and nucleic transgenic plants with improved or altered growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "Gibberellin 2-oxidase AtGA2ox1"
                                                                                                                                                                  Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phillips AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 5; 42pp; English
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                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                              growth inhibition; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characteristics.
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15-JUL-1998;
                                                                                   10-APR-2000
                                                                                                                                                                                                                                                                    Gibberellin
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AAZ55915;
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Sequence 1316 BP; 440 A; 249 C; 252 G; 375 T; 0 U; 0 Other;

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Search completed: December 27, 2005, 18:17:28 Job time : 903.539 secs

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Contact Street BUS4870 corresponding to Gm-r1088-979 (3')
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Project
Public Soybean EST Bush
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Blogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
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/db xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1023-1410"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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BW085298 8aj34h07.
BW1849366 GM880016A
BX814544 Arabidops
BX814574 Arabidops
BX815974 Arabidops
BX815974 Arabidops
BX815974 Arabidops
BX81597 Arabidops
BX814393 Arabidops
BX814030 Br46c09.y
AJ803092 BX8140092
BX814091 Arabidops
BW893076 8am51f05.
BX128566 BX5725608
AL1382874 MtBCTCBC2
DN589159 50141.1 L
B1935635 BX7525608
AV104425 Cam mays
CV292668 BXT881005
BP940509 BR940509
BG646259 ESTF81105
BR9690134 BW690134
                                                                               December 27, 2005, 17:35:38; Search time 6011.88 Seconds (without alignments) 10257.253 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                          82156650
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                              41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM nucleic - nucleic search, using sw model
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BMO85298
BMO85298
CNSOACGN
CNSOACSN
CNSOACSN
CNSOAGN
CNSOAGN
CNSOAGN
AJ803092
BMO8668
BMO89159
                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                     seq length: 0
seq length: 200000000
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Match Length DB
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gb htc:3:*
gb htc:3:*
gb est4:*
gb est5:*
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gb est7:*
gb est7:*
gb gss1:*
gb gss1:*
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1318
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110:
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Maximum DB 6
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	9	305	23		529	7	BG881784	BG881784	sae88£09.
	7	304.2	23	٦.	663	۲.	CV292717	CV292717	EST881094
υ	<b></b>	1.8	22		753	m ·	BI968577	BI968577	GM830005B
	σ,	9.0	22		619		AW584268	AW584268	N210259e
	٥.	9 1	22		789	ın ı	BW685035	BW685035	BW685035
	_	9.7	22		579	9	CA84444	CA84444	EA27D12a
	~	9.	22		724	9	CA844443	CA844443	EA23G12a
U	m	9.	22		517	m i	BP074757	BP074757	BP074757
υ	∢ .	9.4	22		520	m	BP074168	BP074168	BP07
		9.0	57		247	<b>20</b> (	DN982067	DN982067	SV6 43H10
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	۰,	4.	77	٠.	604	- 1	CV630114	CV630114	MGBC60138
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							ALIGNMENTS		
AW184	RESULT 1 AW184969	T T T T	84969	G			ANA CA FRA	יהפחיו	88 - 1111 20 TSR
DBF	DEFINITION	Se 8	se84f09.yl Gm-c1023-14	se84£09.y1 Gm- Gm-c1023-1410	Gm-c1023 (	)23 Bim	23 Glycine max cDNA clos similar to TR:004162 00	SY	MS CLONE ID:
2	MOTORADOR	seq	sequence						
VER	VERSION	AW1	AW184969.1	9.1	GI:6454286	1542	98		
KEY	KEYWORDS	EST.							
SOURCE	URCE	ទីទ	Glycine max	max	(soybean)	ean			
5	KGHINI DIN	E C	arve arvo	Ta :	/iridi	6	Giyeine max Bukarvota: Viridiolantae: Streptophyta: J	Embryophyta: Tr	acheophyta:
		Spe	rmatc	ophyt	a; Ma	gno	Spermatophyta; Magnoliophyta; eudicotyle	rta; eudicotyledons; core eudicotyledons	cotyledons;
		rog	rosids;	enro	side	i;	abales; Fabaceae; Pa	apilionoideae;	Phaseoleae;
0.00	DEFEDENCE	61 <u>7</u>	Glycine.	. 0	ţ	(523)			
A	AUTHORS	Sho	emake	9r.	Kei	E.	Vodkin, L., Erpeld.	ing, J., Coryell	۷.,
į		Kha	nna,	A	3011a,	m	Marra, M., Hillier, L.	, Kucaba, T., M	artin, J.,
		Bec	ς,	Wy.	lie, T.	Þ	nderwood, K., Steptoe	M., Theising, B	, Allen, M.
		BOW	ers,	X	Persor	, B.	Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,	s, M., Pape, D.,	Harvey, N.,
		Sch	urk,		litter	ш	Kohn, S., Shin, T.,	Jackson, Y., Car	denas, M.,
Ě		X C	ann,		Vatere	iton i	R. and Wilson, R.		
Η'n	TITLE	3 E	Public Soybe	Soybe	(1999)	r T	Public Soybean EST Project Humiblished (1999)		
ۇ ك	COMMENT	3 6	Olipubilene Other Este.	מוומרם	1177.	1870	(1999) RIS44870 corresponding to Gm-r1088-979	-r1088-979 (31)	
5	THE	)	í		1		*** ***********************************		

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Fax: 314 286 1810

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

Glone is listed in the 'Other ESTs on clone' field. This clone is

available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

High quality sequence stop: 426.
                                                                                                                                               Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Shoemaker, R., Marra, M., Hiller, L., Kucaba, T., Martin, J., Ranna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Bock, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
Washington Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .566
/organism="Glycine max"
       Glycine max (soybean)
Glycine max
                                                                                                                                  Glycine.
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       SOURCE
ORGANISM
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AUTHORS
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                                        /clone lib="Gm-c1023"
//clone lib="Gm-c1023"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This cDNA library was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (4T) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 TCCACGCCCTTGTTCACGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 CCCACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 cacaragreaargecriscaggaerricggerrerreaageregraageageaggrerreeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 TTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 TTACAGTTCATGGCCAATTTGGAAAACGAAACCTTCGGGTTCTTCAAAAAACCTCAATCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 GAGAAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCA 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 TACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTG 544
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ssue_type="seed coats of greenhouse grown plants"
b_host="DH10B"
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Pred. No. 2.7e-111;
0; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.2%;
Matches 499; Conservative
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                                                                                                                                                                                                                                                                                                                                                      245 TIGGAGITAARIGGCCAATITIAGAAAACGAGGCCCTCAGGTICTTTAAAAAATCTCAGTCC 304
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                                                                                       65 ACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTGAAACCATTCAAG
                                                                                                                                   15 ACAATGGTTGTTTTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAG
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                                           Gaps
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0
Length
                                           Indels
Score 444.8; DB 3;
Pred. No. 5e-108;
0; Mismatches 67;
Query Match 33.7%;
Best Local Similarity 87.9%;
Matches 485; Conservative
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BM085298 556 bp mRNA linear EST 23-JUL-2004 saj34h07.yl Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA

LOCUS

GI:16995926

BM085298.1 BM085298.1 EST.

ACCESSION VERSION KEYWORDS

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AAAGAATTCACATGGTGGGAATACAAGAAGGCTGCGTATGCGTCAAGGCTAGCGGATAAT
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/mol_type="mRNA"
/db_xref="texon:3847"
/clone="Gm-r1088-5828"
/clone_lib="Gm-r1088-5828"
/note="The library Gm-r1088 is a sequence-driven, reracked set of 9,216 low redundancy clones selected from cDNA libraries from various tissues and stages of development of soybean that consists of 2,706 cDNAs from germinating cotyledons (source library Gm-c1027); 1,355 cDNAS from
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GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewin, H. A., Director, Keck Center for Comparative and Functional
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                                                                                                                                                      CCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAAC 484
TTAGAGTTCATGGCCAATTTGGAAAACGAAACCCTCAGGTTCTTCAAAAAACCTCAGTCC 254
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Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                           AACGGCGATGTCGGTTGGGTCGAATACCTCCTTCTCCAACCCCAACCCTGACGTCATCTCC
                                                                                                                                                                                                                                                                                          AACGGTGATGTCGGTTGGGTCGAATACCTCCTCAACACACCAACCCTGATGTTATCTCA
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Other ESTS: BG881784 corresponding to Gm-c1065-2970 (5')
Contact: Vodkin, L.O., Pl. A Functional Genomics Program for Soybean (NSF 9872565)
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immature seed coats (libraries Gm-c1019 and Gm-c1023); 917

CDNAs from tissue culture derived somatic embryos (source libraries Gm-c1036, and Gm-c1075); 3,275 cDNAs from

germinating seedlings, shoot tips, or leaves exposed to various stresses (source libraries Gm-c1064, Gm-c1065, Gm-c1066, and Gm-c1067); and Gm-c1067, and Gm-c10074, and gercines from be dingal pathogens (source libraries Gm-c1067), and Gm-c1074). The Syoung leaves exposed to bacterial and fungal pathogens was used to select singletons, or a representative of each contig, which were reacked to form library Gm-r1088 and the cDNA clones of the reacked Gm-r1088 library were then sequencing was funded by NSF Plant Genome project #9872565 (http://soybeangenomics.cropsci.uiuc.edu/) as part of creation of a low redundancy soybean cDNA set. The source CDNA libraries were constructed by the laboratories of illa vodkin, University of Illinois, Randy Shoemaker, lowa State University, and Paul Keim, Northern Arizona University as part of the Public EST project, to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://web.ahc.um.edu/blodata/nsfsoy/, Reracking and 3' sequencing were conducted by services of the University of Illinois Keck Center for Computational Genomics and Bioinformatics, university of Minnesota, sequencing were conducted by services of the University of Illinois Keck Center for Computational Genomics and library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."

88; Indels 11; Gaps Length 622; 32.6%; Score 430; DB 5; L 84.1%; Pred. No. 4.9e-104; ive 0; Mismatches 88;

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670 502 AACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAA----CCGGAATTTGGTTGGGTTT

730 442 GGGGAGCACACACACACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTG

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**ATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAAGCAT** 

850 322 910

ATCAATGTTGGTGACACTCTACAGGTGATGACTAATGGGGAGGTTTAAAAGTGTAAAGGAT AGGGTTTTGGCTGACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCG TTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTAC

970

AAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAAT 1030 ricacicadadacararcacciriraccircicarciradadecacacararrana 202

142

1031 AGGCTTGCCCCTTTCCAGAATCTGCTGCTGATTAACCAAACACCCCTTCAAA----T 1085

us-10-670-454-1.rst

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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH78ZH09 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

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Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                   HTC 06-FEB-2004
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/ecotype="Col-0"
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Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/clone="GSLIFB7ZE01"
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Submitted (18-NOY-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr. if the sequences are based on single pass reads.

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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L Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)

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                                                                                                          Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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[ [bases 1 to 1362]
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ecotype="Col-0"
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Pred. No. 7.8e-103;
0; Mismatches 317;
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/db_xref="taxon:3702"
/clone="GSLTPGH78ZH09"
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66.3%;
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EXELSTY4.1 GI:42471555
HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1363)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,
Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH20ZC07 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                            TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          br 191 1000 Entra ceuts. France (Enual) : Sequence constructions to the sequences are based on single pass reads.

Genoscope members carried out sequencing and annotation : Castel V., Mary J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 prime are assembled with Phrap.
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Location/Qualifiers
                                                                   GCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                                  1062 GAGAAACAACCICTICTCAATCATAAAACCCTTGIATGAAAGTAGICAI 1110
                                                                                                                                                                                                                                                     1046 CAGAAATCTGCTGCTGATTAACCAAACACCCTTCAAATTCCACTCAT 1094
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/db_xref="taxon:3702"
/clone="GSLTPGH20ZC07"
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            Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 GTGTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAAGGGACACT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626 CCTTGCCCTGAGGTGCAAGCACTGAACCGGAATTTGGTTTGGGTTTTGGGGAGCACACAGAC 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702 CCACAGATAATCTCAGTGCTAAGATCTAATAACACGGCGGGTCTTCAAATCTGTGTGAAA 761
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                                                                                                                                 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
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Pred. No. 5.4e-102;
0; Mismatches 319;
                                                                                                                                                                                                         organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB20ZE08"
/tissue_type="Flowers and
  URGV INRA : Clepet C., Caboche M.
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Castelli

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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 ENRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - The sequences are based on single pass reads.

The sequences are based on single pass reads.

Infe Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                    Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; rosids; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1339)

Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,P., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

Mhole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genoscope.cns.fr/cg1-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
 BX814383.1 GI:42472054
HTC; GSLT CDNA.
Arabidopsis thaliana (thale
Arabidopsis thaliana
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                                                                                                                                                                        Score 386.4; DB 4;
Pred. No. 3e-92;
0; Mismatches 281;
/mol_type="mRNA"
/db xrefe="taxon:3702"
/clone="GSLTFB70ZF11"
/tissue_type="Flowers and bu
/ecotype="Col-0"
                                                                                     /plasmid="pCMVSPORT_6"
                                                                                                                       /gene="At1g30040"
                                                                                                                                                                          29.3%;
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Matches 581; Conservative
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DEFINITION RESULT 8 CNSOAC3R

LOCUS

CNSOAC3R

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB70ZF11 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION

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AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 5 05 018, mRNA sequence.
  57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 378.6; DB 2;
Pred. No. 3.2e-90;
0; Mismatches 54;
                                                                                'organism="Glycine max"
                     High quality sequence stop: 413.
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Best Local Similarity 88.4%;
Matches 411; Conservative (
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Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
134 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
When it has been determined, an EST from the other end of this when it has been determined, an EST from the State of this clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EBBUZJUJ GR-C1051 Glycine max CDNA clone GENCME SYSTEMS CLONE ID: Gm-C1051-1097 5' similar to TR:O64692 O64692 PUTATIVE GA4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, R.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         970 GCACCATTGCCATTGCCTTGTCCCTGAGCAAGATGATTTGTGCTTTACAAAGAATTCACT 1029
CGTCAAACCCCTCAAATTTTCCGTGAGTCGGTGGAGGAGTACATGAAGGAGATTAAGGAA 552
                                          565
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                                                                                                                                               613 CTGAGTAAAATGCTGAGAGAGAGAGAGAGTGACTCGTGCCTGAGACTAAACCATTATCCG 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910 ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCGCCATTGAGCCAGAAGATC 969
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                                        ATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGGATAAGGCAGAATACG
                                                                                553 GTGTCGTACAAGGTGTTGGAGATGGTTGCCGAAGAACTAGGGATAGAGCCAAGGGACACT
                                                                                                                                                                                                                                                                                       CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
                                                                                                                        TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCG
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When you was genoscope.comes its angle pass reads.

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J. W., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fi/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1128)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craud, C., Quetler, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                         linear HTC 06-FEB-2004
                            TGTTTGTACAAAGAGTTCACATGGTGTAATACAAGAGGCTGCGTACACTTCAAGGCTA 1021
                                                    677 AGCTTGTACAAGGAATTTACTTGGTTTGAGTACAAAAAATCTGCTTATAATCAAGGCTGG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                    from clone
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                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana Full-length cDNA Complete sequence from clossITFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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1. .1128
/organism="Arabidopsis thaliana"
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/ecotype="Col-0"
/plasmid="pcMVSPORT_6"
                                                                                                                           GCTGATAATAGGCTTGCCCCTTT 1044
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/db_xref="taxon:3702"
/clone="GSLTFB56ZG10"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCTCAACACCCAACCCTGATGTTATC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482 AACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 GATTATGTTTCTGCAGTAAAGAGAATGGCGTGTGAGATTCTTGAAATGTTGGCTGATGAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAGTGATTCG 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGGGTTTGGGGAGCACACACACACAGATAATTTCTGTCTTAAGATCTAACAGCACA 721
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                                                                                                 1 (bases 1 to 785)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H.
Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 ATCGGGTTTTGGTGACTACTGACCCGCAAATAATATCGGTTTTTGAGATCCAACACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCGAGAAAGACAGAGCTGCTCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGC
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Pred. No. 4.5e-84;
0; Mismatches 232; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Antirrhinum majus"
/mol_type="mRNA"
/db xref="kaxon:4151"
/db xref="taxon:4151"
/tissue="1018 5 05 018"
/tissue type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                  Contact: Schwarz-Sommer Z
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zucchtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                                                                                                                                                                                                             DEFICIENS
Plant Cell 16 (12), 3197-3215 (2004)
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                                                                               Antirrhinum.
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/lab unbea="untue"
/clone lib="Gm-c1069"
/note="Vector: pBluescript II SK+; Site I: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site I: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etiolated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoRR). This
                                                                          Shoemaker, R. , Kaim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCan, R., Waterston, R. and Wilson, R.
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: 40RP from Gibco
High quality sequence stop; 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 TCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCCGATGCCAAGAAT 184
     osids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGGAGITAAIGGCCAAITIAGAAAACGAGGCCCICAGGIICTITAAAAAAICICAGICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="Degenerating cotyledons, 9-10 day etiolated seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1069-2961"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 336.2; DB 3
Pred. No. 7.7e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
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al Similarity 88.4%;
365; Conservative
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Best Local Similarity
Matches 365; Conserv
                               Glycine
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                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963 GTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAG 1022
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311
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                                                                                                                                                                                                                                                                                                                431
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                                                                                                                                                                                                                                                                                                                                                                                                                       491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 TATTTCCAAGTCTTCTCAAAAGCCCGGGAACTTTCAGAAACGCATTGGAAGAGTACACAA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           861 GACCTTCATTGACTCAGAGAATCGCTCCGTTCACATGTTTGATAGACAATGAGGACGAGA 920
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Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                                                                                         TAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 CATCAGTGAGAAAAATGACATTCGATGTTTTGGAGAAGATCACAGATGGGCTAGGGATCA
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/dev stage="harvested 3 weeks post inoculation with Glomus intraradices"
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MEBC10E02F1 MtBC Medicago truncatula CDNA clone MtBC10E02 T3, mRNA
                                                                    241 TATTGATGGATGAAAGAGCGACTCTGTTTTCAGGCTGAATCACTATCCTCCATGTCCTG 300
                                                                                                                                                                                                             301 ATATTCAAGAATTCAATGCCAAAATTTAATTGGATTTGGAGAACATACTGATCCACAAA 360
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire (

Biologie Moleculaire des Relations Plantes-Microorganismes,

CNRS.INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:

Mt-est@toulouse.inra.fr Website:
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1 (Dasses 1 to 478)

Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from endomycorrhizal roots

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTAC
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Location/Qualifiers
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/clone="MtBC10E02"
/tissue_type="arbuscular_mycorrhiza"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  993 ACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAA 1029
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/cultivar="Jemalong"
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/note="Vector: pBluescript SK(-); Site 1: BCORI; Site 2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and img/ml 2, 40 (pHS.8).
Presh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
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Lycopersicon esculentum
Elycopersicon esculentum
Elycopersicon esculentum
Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 694)
Van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,
Ronning, C. and Tanksley, S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                   BI208568 600 Lycopersicon esculentum cDNA clone cTOS17020 5' end
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                                      424
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Location/Qualifiers
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0; Mismatches 206; Indels
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/organism="Lycopersicon esculentum"
/mol type="mRNA"
/cultivar="TA496, E6203"
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/lab_host="SOLR"
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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/done libe-Late Blight-Challenged Tubers"
/done libe-Late Blight-Challenged Tubers
/note="Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were incculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
            Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S. Generation of ESTB from late blight-challenged potato tubers (Dnpublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 AGTAAGCTTTTAATGGATGAAAAAGTGATTCACTTTTTAGGCTAAATCATTACCCTCCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 IGTCCTGATGAATTTCAAGAATATAATGGAAGAAATTTAATTGGATTTGGTGAACATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 GACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 TACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACAAATCACTTTGCATTTTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 TACATTCTTTTGTCAACAATTCTGAGTTCAATTACCAAAAATTTGCATCTATTTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 GTCAATCCAAAGATATAAGAGATGCTGTGAATGATTATGTATTAGCAATGAAGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 TGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGGGATAAGGCAGAAGAATACGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 GCTTGTGAGATTCTTGAAATGTTAGCAGAGGGATTAAAAATTCATCCAAAGAATGTATTT
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                                                                                                                                                                                                                                                                                                             /organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Shepody"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4113"
/clone="50141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                       1. .893
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/note="Vector: pBluescript pSK; Site 1: ECORI; Site 2: XhO1; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil: 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPA8). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. CDNA was prepared from poly4+ enriched RNA. The CDNA was prepared from poly4+ enriched RNA. The CDNA was prepared from poly4+ enriched RNA. The cDNA was preased from poly4+ enriched RNA inserts were ware extracts. Plasmids containing cigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
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50141 5', mRNA sequence.
DNS89159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viriliplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 893)
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25.3%; Score 332.8; DB 1; Length 478;
Best Local Similarity 83.0%; Pred. No. 6.1e-78;
Matches 395; Conservative 0; Mismatches 72; Indels 9
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<sup>1040</sup> CCTTTCCAGAAA 1051 | | | | | | | | | | | 723 CTATTTGAGAAA 734

Search completed: December 28, 2005, 00:38:43 Job time : 6016.88 secs

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	Description	Sequence 1, Appli	Sequence 62, Appl	Sequence 13, Appl	'n	7,	Sequence 64, Appl	ď	7,	'n	Sequence 3, Appli	ų,	Sequence 67, Appl	Sequence 71, Appl		68,	58	5,	6	Sequence 3, Appli	4	12,	1,	26,	57,
SUMMARIES	ΙD	US-09-719-108-1	US-09-371-307-62	US-09-614-912-13	US-09-614-912-5	US-09-719-108-7	US-09-371-307-64	US-09-719-108-9	US-09-614-912-7	US-09-719-108-5	US-09-614-912-3	US-09-614-912-1	US-09-371-307-67	US-09-371-307-71	US-09-371-307-66	US-09-371-307-68	US-09-371-307-58	US-09-371-307-70	US-09-614-912-9	US-09-719-108-3	US-09-719-108-4	US-09-614-912-15	US-09-614-912-11	US-09-371-307-56	US-09-371-307-57
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Patent No. 6670527
GENERAL INFORMATION:
GENERAL THORMATION:
GENERAL THORMATION:
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: CO00-12-08
PRIOR APPLICATION NUMBER: EPT/GB99/01857
PRIOR PELING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR PELING DATE: 1998-06-15
PRIOR PELING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING VEY: 2.1 Query Match
100.0%; Score 1318;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1318; Conservative 0; Mismatches ; TYPE: DNA ; ORGANISM: Phaseolus coccineus US-09-719-108-1 LENGTH: 1318 RESULT 1 US-09-719-108-1 셤 ઠે ద ò ద Š ઠે ઠે

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Query Match 67.8%; Score 893.8; DB 3; Best Local Similarity 84.9%; Pred. No. 1.5e-255; Matches 1069; Conservative 1; Mismatches 158;
                                                         APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Hiller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Roa, Sudabathula
APPLICANT: Logusch, Sherry J.
TILE OF INVENTION: Methods for controlling gibb
FILE REFERENCE: MOBT: 1999-08-10
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEC ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEC ID NO 62
LYPE: DNA
TYPE: DNA
TYPE: DNA
                Sequence 62, Application US/09371307A Patent No. 6723897 GENERAL INFORMATION:
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Gaps

265

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174

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AGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTGAGATACAAGAAGGCTGCGTACACTTC 1014
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                                                                                                                        Length 1352
                                                                                                                                                           Indels
                                                                                                                     Score 430.8; DB 3;
Pred. No. 1.2e-117;
0; Mismatches 332;
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larity 65.7%;
Conservative
   Microsoft Office
; SOFTWARE: Microsoft; SEQ ID NO 13
; LENGTH: 1352
; TYPE: DNA
; ORGANISM: Glycine m: US-09-614-912-13
                                                                                                                                         Similarity
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Best Local S
Matches 665
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Gou-Hau
APPLICANT: Miao, Gou-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Ee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Gonai, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: B1378 US NA
CURRENT PEPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-15
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
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Patent No. 6677502
GENERAL INFORMATION:
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US-09-614-912-13
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                 TGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGGCGGT
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                                                          513 ACACAACT------TCTCTGTTTATGGCAAAAACCCTGAGAATTCAGGTGTCT
                                                                                                    GGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGC
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Patent No. 6670527
GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 2000-12-08
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PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
PRIOR PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver: 2.1
LENGTH: 1237
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ORGANISM: Arabidopsis thaliana
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US-09-719-108-7
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Pred. No. 3.7e-117;
0; Mismatches 333;
                                                                                                                                                                                                                                                                                                                APPLICANT: Miao, Gou-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Eamodu, Omolayo O.
APPLICANT: Eakal, Hajime
APPLICANT: Sakal, Hajime
APPLICANT: Sakal, Hajime
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,650
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,956
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                          Sequence 5, Application US/09614912
Patent No. 6677502
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ilarity 65.6%;
Conservative
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Rafalski, Antoni
Orozco, Buddy
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LENGTH: 1365
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Best Local S
Matches 664
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US-09-371-307-64
Sequence 64, Application US/09371307A
Patent No. 6723897
GENERAL INFORMATION:

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AACAGCACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCT

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TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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379 CGGCACACCCCTGCAATTTTCAGAGAGGCAGTGGAAGAGTACATTAAAGAGATAGAAGAGA 438
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                                        ATGTGCTATGCGGTGTTGGAATTGATGCCGGAGGGGTTGGGGGATAAGGCAGAGGAATACG
                                                                                 <u> ATGTCGAGCAAATTTCTGGAAATGGTAGAGGAAGAGCTAAAGGTAGAGCCAAAGGAGAAG</u>
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APPLICANT: Miao, GOU-Hau
APPLICANT: Famodu, Omolayo O.
APPLICANT: Ee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Gaimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
FILE REFERENCE: BB1378 US NA
FILE REFERENCE: B91378 US NA
FILE REFILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
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                                          206
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                                                                                   892
                                                                                                               899 TITCGAAGIGGAAACACAGAGTITIGACAAATGGAITIAAGICTAGACTCTCAATGAIT 958
                                                                                                                                                                  TACTTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAA 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 ATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG 205
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                           TITIAAAAGTGTAAAGCATAGGGTTTTTGGCTGACACAAGGAGTCAAGGTTATCAATGATC
                                                                                                                                                                                                                                                                         GATCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGG
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Pred. No. 2.1e-103;
0; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09719108
Patent No. 6670527
GENERAL INNORMATION:
GENERAL INNORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Phillips, Andrew L
ITILE OF INVENTION: Gibberellin 2-Oxidase;
FILE REPERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: US/09/719,108
FILE REPERENCE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SSEQ ID NOS: 16
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ORGANISM: Arabidopsis thaliana
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64.1%;
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Best Local Similarity 64.1
Matches 595; Conservative
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LENGTH: 1008
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  960 AGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGC
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27.1%; Score 356.6; DB 3; Length
Best Local Similarity 63.2%; Pred. No. 1.5e-95;
Matches 586; Conservative 0; Mismatches 329; Indels
                                                                                           1020 TAGCTGATAATAGGCTTGCCCCTTTCCAGA 1049
                                                                                                                                    1070 regegekakakakekerrekerrekakan 1099
                                                                                                                                                                                                                                                                                                                    APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
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NAME/KEY: misc_feature
LOCATION: (1243, 1265)
OTHER INFORMATION: unidentified residue
US-09-719-108-5
                                                                                                                                                                                                                               US-09-719-108-5; Sequence 5, Application US/09719108; Patent No. 6670527
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                            Length 1473;
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Pred. No. 1.4e-97;
0; Mismatches 374; Indels
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
                                                                                                                                                                                                          27.6%;
al Similarity 61.3%;
607; Conservative
                                                                                                                 TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-614-912-7
                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 607; Conserv
                                                                                             LENGTH: 1473
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                                                                                 TTAATCACTATCCACCATGTCCTCTTAGCAATAAGAAACCAATGGTGAAGAATGTGA
                                                                                                                           TTGGGTTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACAT
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                                          TGAACCACTACCCCTTGCCCTGAGGTGCAAGCACTGAAC
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APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REPERENCE: BB1379 G US
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR PELLOR DATE: 1999-07-12
PRIOR PELLING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PLING DATE: 1999-12-15
PRIOR PLING DATE: 1999-12-15
PRIOR PLING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
SPIOR APPLICATION NUMBER: 60/172,946
PRIOR PILING DATE: 1999-12-21
SPIOR PILING DATE: 1999-12-21
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Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Caimi, Perry G
Anderson, Shawn
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CRGANISM: Oryza sativa
US-09-614-912-3
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US-09-614-912-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 CCTGCACCGTCCCGTCCTGCG-----CGGTCTTCCGGGCCGCTCTGAACGAGTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             783 rechantegeericegeaceaceareaciericeirecereceaceaceaceareirer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 GCGTGAACCACTACCCCCCCGCCCCCCAGGGGCTCGGCTGCAGCGTCACCGGCT
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                                                                   6
      Length 1650
                                                                0; Mismatches 375; Indels
   Score 354; DB 3;
Pred. No. 1e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1029 ATAGGCTTGCCCCTTTCCAGAA 1050
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26.9%;
60.9%;
Query Match
Best Local Similarity 60.99
Matches 598; Conservative
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943 TTCGCGGGGCCGCCGCTGGGGCAGCGGATCGCGCCCTGCCGCAGGTGCTGGCGGAGGGA 1002
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599 TCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAACCGGAAT 658
                                                                                                                                                                                                                                                                   643 CAGGTGTTCCGCGTGAACCACTACCCGCCCTGCCCGCGCTGCAGGCCTGCAGC 702
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                                                                                               GGGTTGGGGATAAGGCAGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGAT 598
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Pred. No. 4.4e-82;
0; Mismatches 170; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1016 AGGCTAGCTGATAATAGGCTTGCCCCTTTCCAGAA 1050
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23.6%;
Best Local Similarity 70.1%;
Matches 441; Conservative
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ORGANISM: Gossypium hirsutum
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US-09-371-307-67
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US-09-371-307-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CCGGGCCCCAGGGACAGCTTCTCGGGAGTGCCGGTCGTCGACCTGTCCAGCCACCACCAGCGACGCG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAACCACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 24.0%; Score 315.8; DB 3; Best Local Similarity 58.9%; Pred. No. 2.4e-83; Matches 586; Conservative 0; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caiml, Perry G
APPLICANT: Caiml, Perry G
APPLICANT: Caiml, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: 06/143,401
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-13
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR PILING DATE: 1999-12-21
PRIOR PELING DATE: 1999-12-21
                                                                                            Sequence 1, Application US/09614912
Patent No. 6677502
GENERAL INFORMATION:
                                                                                                                                                                                    Allen, Steve
Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Microsoft Office 97
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SOFTWARE: Microsoft O
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                                RESULT 11
US-09-614-912-1
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965 TIGIACAAAGAGTICACAIGGIGIGAAIACAAGAAGGCIGCGIACACTICAAGGCIAGCI 1024
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                                                                                                                                                                                                                                                                                                    TTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 rrcrrcercaacerceccaacacccrecaestrreaceaaceaecercaesecere
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| Patent No. 6723897
| GENERAL INFORMATION:
| APPLICANT: Broam, Sherri M. |
| APPLICANT: Broam, Sherri M. |
| APPLICANT: Piler, Kenneth J. |
| APPLICANT: Kishore, Ganesh M. |
| APPLICANT: Kishore, Ganesh M. |
| APPLICANT: Logusch, Eugene W. |
| APPLICANT: Logusch, Eugene W. |
| APPLICANT: Logusch, Sherry J. |
| APPLICANT: Logusch, Sherry J.
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                                                               Indels
al Similarity 55.8%; Pred. No. 7e-39; 316; Conservative 0; Mismatches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 GATAATAGGCTTGCCCCTTTCCAGAA 1050
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NAME/KEY: unsure
LOCATION: (178)
CTHER INFORMATION: n = a,
US-09-371-307-66
      Best Local Similarity
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US-09-371-307-66
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                                                                     Matches
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                                                                                                                                                                                                                                                                                                                577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578 CTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          412 GGTGACTCCTTACAGGTAATGACCAATGGAAGGTTTAAAAGGTGTAAAACATAGGGTAGTG 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 ACTTGGTTCGAGTACAAGAATCTGCTTATAATTCCAGATTGGCAGATAATAGGCTCATT 651
                                                                                                                                                                           52 CAAACTITGAGGGTGGCTTTGAATAATTATGAAATCAGTAAAGAAAATGGCGTGTGAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 TTGATGGATGAAGAGAGACTCTGTTTTCAGGGTGAATCATTACCCACCATGCCCTAAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 Gricaaccrirgagregraarescaarescaaresesarerisarresarrirgarrisareacae 291
                                                                     CATCATTTCAGGGCGGTGGTGGAGAACTACATTACAGCAGTGAAGAACATGTGCTATGCG
                                                                                                                                                                                                                                                                                                                518 GTGTTGGAATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGCAAGCACTG-------AACCGGAATTTGGTTTGGGTTTGGGAGCAC
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: APPLICANT: MOBE: 216
CURRENT APPLICANT: NUMBER: US/09/371,307A
SEQ ID NOS: 89
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 71
LENGTH: 811
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US-09-371-307-71
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US-09-371-307-71
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                                                                284 TTCTTTAAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCCGGACCCTTTCGGCTAT
                                 Gaps
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APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Kiehereh J.
APPLICANT: Kiehere, Ganesh M.
APPLICANT: Ried, Ganesh M.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Ream, Joal E.
APPLICANT: Ream, Joal E.
APPLICANT: Loquach, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 406
                                 12;
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Pred. No. 1e-35;
0; Mismatches 113; Indels 27;
   Length 403;
                                 Indels
Query Match 11.8%; Score 155.6; DB 3; Best Local Similarity 63.2%; Pred. No. 5.8e-36; Matches 261; Conservative 0; Mismatches 140;
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66.6%;
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NAME/KEY: unsure

LOCATION: (306)

CHER INFORMATION: n = a, c, US-09-371-307-68
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Best Local Similarity 66.6
Matches 279; Conservative
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Search completed: December 28, 2005, 00:46:40 Job time : 272.271 secs

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Sequence 1350, Ap
Sequence 1350, Ap
Sequence 64, Appl
Sequence 21951, A
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Sequence 78659, A
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Sequence 6183, Ap
Sequence 141, App
Sequence 9278, Ap
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Sequence 62, Appl
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Sequence 7, Appli
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Sequence 16086, A
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                                                                                     December 27, 2005, 17:51:22 ; Search time 1238.83 Seconds (without alignments) 8797.858 Million cell updates/sec
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/ cgn2 6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-401-321-62

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US-09-931-842A-1350

US-10-401-321-64

US-10-401-321-64

US-10-670-454-5

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US-10-670-458-5

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US-10-425-114-6183

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Sequence 159585, Sequence 103352, Sequence 103352, Sequence 1288, Ap Sequence 101563, Sequence 177171, Sequence 177171, Sequence 77, Appl Sequence 71, Appl Sequence 71, Appl	Sequence 66, Appl Sequence 68, Appl Sequence 68, Appl Sequence 58, Appl Sequence 58, Appl Sequence 453, App Sequence 67680, A Sequence 20123, A Sequence 20123, A Sequence 20123, A Sequence 20123, A
US-10-425-115-159585 US-10-425-115-103352 US-10-427-115-103352 US-10-427-599-128662 US-10-424-599-101563 US-10-425-114-34429 US-10-425-115-17771 US-10-401-321-71	US-U9-171-307-66 US-U9-371-307-66 US-10-401-321-68 US-10-401-321-68 US-10-401-321-58 US-10-401-321-58 US-10-424-599-67680 US-10-424-599-67680 US-10-424-599-42166 US-10-424-599-108868
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201.8 188.6 188.6 187.2 187.2 172.2 169.8 166.8	155.6 155.6 154.8 152.4 150.4 146.4 123.8 123.8
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## ALIGNMENTS

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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                     CENERAL INFOGRALIANT STROMAGE, Stephen G
APPLICANT: Thomag, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TILE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR PILING DATE: 2000-12-08
PRIOR PILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 981281.8
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 1
            Sequence 1, Application US/10670454 Publication No. US20040229357A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1318; Conservative
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Sequence 3, Application US/10821711

Sequence 3, Application US/10821711

Sequence 3, Application No. US20040237142A1

GENERAL INFORMATION:
APPLICANT: Gilberteon, Larry A
APPLICANT: Krieger, Elysia K
APPLICANT: Ye, Xudongen
APPLICANT: Zhang, Wanggen
TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS
FILE REFERENCE: 38-21 (52967) B
CURRENT APPLICATION NUMBER: US/10/821,711
CURRENT APPLICATION NUMBER: 004-04-08
PRIOR FILING DATE: 2004-04-08
PRIOR FILING DATE: 2003-04-09
SEQ ID NO 3: 16

LENGTH: 999
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Phaseolus coccineus
                                RESULT 2
US-10-821-711-3
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Best Local S:
Matches 999,
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Db 339 GAGABAGGCTGGTCCCCTGACCCTTTTGGCTACGGCAGGAGGATTGGCCT 398  Qy 365 AACGGTGATGGGTCGGATGGATACCTCCTCCTCTCAACCCAACCCTGATGTTATCTCA 424	Db 399 AACGGGATGTCGGTTGGGTCGATACCTCCTCTAAACCAACC	Db 459 CCCAAGTCACAGTTCATTTCAGAGAAGTCCTCAGAATTTCAGGGCGGTGGTGGAGGAA 518 Qy 485 TACATTACAGCAGTGAAGAACATGTGCTTATGCGGAATTGATGGGGGGTTG 544	519	Db 579 GGGATAACGCAGAGGAATGTGTTGAGTAGGTTGCTGAAGGATGAGAAGAGTGTTCC 638  Qy 605 TTCAGGTTGAACCACTACCGGCCTTGCCCTGAGGACTGAAGCACTGAACCGGAATTTG 661	639	Db 699 GTTGGATTGGAAGGAACCAACAAATTTTGTTTTTTTTTT	Qy 722 TCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACT 781	Qy 782 TCCTTTTTCATCATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGT 841	Qy 842 GTAAAGCATAGGGTTTTGGCTGACGAAGTCAAGGTTATCAATGATCTACTTTGGA 901	Qy 902 GGACCAGCGTTGAGTGAAAATATAGCACCTTTAACCTTCAGTGATGTTAAAAGGAGAGAG 961	OY 962 TGTTTGTACAAGAGTTCACATGGTGTAATACAAGAAGGCTGCGTACACTTCAAGGCTA 1021	108		Qy 1133 TCTTTCCTGTGTCTGGGTTTCAAACAGTTGACTCTACTTGACATATAAGAAAT 1192		OY 1242 TAACAGTTGGTCTCAACTTCCCTTTCCTCAATGGAAGGCAACTCTAGTTACA 1300	RESULT 4 US-10-401-321-62 Sequence 62, Application US/10401321 Enablication No Hesphanes	; GENERAL INFORMATION: ; APPLICANT: Brown, Sherri M.
QY 728 TIGCAMAICTGICICACAGAIGGCACTIGGGTITCAGICCCACCIGAICAGACTICCTIT 787	OY 788 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG 847 	OY 848 CATAGGGTTTTGGCTGACACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 907	Oy 908 GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGTGTTTG 967	Qy         968         TACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT         1027           Db         901         TACAAAGAGTTCACATGGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT         960	Qy 1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGATTAA 1066		ωo	J	; APPLICANT: Kishore, Ganesh M. ; APPLICANT: Blich, Tedd D. ; APPLICANT: Logusch, Eugene W. ; APPLICANT: Rao, Sudabathula			; SEQ 1D NO 62; ILENCTH: 1359; TYPE: DNA; ORGANISM: Glycine max	Query Match  Best Local Similarity 84.9%; Pred. No. 1.7e-250; Matches 1069: Conservative 1: Mismatches 158: Indels 31: Gaps 5:	AGCCAGCATTAAACCAGTTTTTCCTTCTGAAACCATTCAAG 12	125 TCCACGCCTTGTTCACGGGGATTCCTGTGGTCGACGTCACGACCCCCGATGCCAAGAAT	185 CTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTCAAGCTTGTGAACCATGGTGTTCCA 	OY 245 TIGGRGTIAANGGCCAATITAGAAAGGGGCCCTCAGGTTCTTTAAAAATCTCAGTCC 304	Oy 305 GAGAAAGACAGAGCTGGTCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGGCCCA 364

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Publication No. US20040229357A1
GENERAL INRORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Helden, Peter
TTILE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION WUMBER: US/10/670,454
CURRENT FILING DATE: 2003-09-26
FRIOR APPLICATION NUMBER: US/09/719,108
FRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-06-12
FRIOR FILING DATE: 1998-06-15
FRIOR FILING DATE: 1998-07-15
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; ORGANISM: Glycine max
US-10-401-321-62
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                                                                                                                                                                                                                                                            Length 1026;
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                                                                                                                                                                                                                                                            Score 425.4; DB 3;
Pred. No. 2.8e-113;
0; Mismatches 306;
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 1026
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                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
                                                                                                                                                                                                                                                                            Best Local Similarity 66.8
Matches 622; Conservative
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US-09-938-842A-1350

Sequence 1350, Application US/09938842A

Sequence 1350, Application US/09938842A

Sequence 1350, Application US/09938842A

GENERAL INFORMATION:

APPLICANT: Kreps, Joel

APPLICANT: Kreps, Joel

APPLICANT: Trang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            976 GCACCATIGCCATGCCTTGTCCCTGAGCAAGATTGGCTTTACAAAGAATTCACTTGG 1035
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       GACTICGGCTICTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTA
                            GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC
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                                 CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
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Sequence 64, Application US/09371307A

Patent No. US20020053095A1

GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Filer, Kenneth J.
APPLICANT: Kishore Ganesh M.
APPLICANT: Kishore Ganesh M.
APPLICANT: Ream, Joel B.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: ApplicANT: New Only Selection Interest APPLICANT: USY085:216

TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: WOSE:216

CURRENT APPLICATION NUMBER: US/09/371,307A

CURRENT FILING DATE: 1999-08-10

NUMBER OP SEQ ID NOS: 89
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SEQ ID NO 64
LENGTH: 1403
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Best Local Similarity
Matches 669; Conserv
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Publication No. US20040009476A9

GENERAL INFORMATION:

APPLICANT: HATCHEN, Joel

APPLICANT: WANG, Xun

FILE REFREENCE: SCR.P1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR APPLICANT: WANG, Xun

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

FEAST OF WANG, Xun

FEAST OF WANG, X
                                                             986 TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC 1045
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368 GCACCATTGCCATGCCTTGTCCCTGAGCAAGATGGTTGGCTTTACAAAGAATTCACTTGG 927
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Pred. No. 2.8e-113;
0; Mismatches 306;
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Matches 622; Conservative
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                                                                                                                                                                                           Length 1403;
APPLICANT: Logusch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11999.0216. DVUSG1 (MOBT:216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
SEQ ID NO 64
LENGTH::1403
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                           32.2%; Score 424.8; DB 6;
larity 66.0%; Pred. No. 5e-113;
Conservative 0; Mismatches 327;
                                                                                                                                       ; TYPE: DNA
; ORGANISM: Glycine max
US-10-401-321-64
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                                                             TACTTTGGAGGTCCACCATTGAGTAGAAAATAGTACCATTATCTTCACTTATG---AAA
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                                            CATGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAA
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Sequence 64, Application US/10401321
Publication No. US20030233679A1
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Hiller, Kenneth J.
APPLICANT: Kilshore, Ganesh M.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Ream, Joel E.

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                                                    632 AGAAGGGTTGAAGATTCAGCAAAAGGATGTGTTTAGCAAGCTTCTAATGGATAAACAAAG 691
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535 GGAGGGGTTGGGGATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAG
                                                                                                               595 TGATTCGTGCTTCAGGTTGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAACCG
                                                                                                                                                     692 TGACTCTATTTTCAGGGTGAATCATTACGCTGCTTGTCCTGAAATGACTCTGAATGATCA
                                                                                                                                                                                                                           655 GAATTIGGITGGGTITIGGGGAGCACACACACACACAGATAATTICTGICTIAAGAICIAA
                                                                                                                                                                                                                                                            752 GAACTIGATIGGGITTGGAGAACACACACACACAAAATCAICTCTGTIAAGAICCAA
                                                                                                                                                                                                                                                                                                                                                                           775 TCAGACTTCCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                895 CITIGGAGGACCAGCGTIGAGIGAAAATATAGCACCTITACCTICAGIGATGTTAAAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-6/0-454-9

US-10-6/0-454-9

SQUEENCE 9, Application US/10670454

Publication No. US20040229357A1

GERREAL INFORMATION:

APPLICANT: Thomas, Stephen G

APPLICANT: Hedden, Peter

APPLICANT: Phillips, Andrew L

TITLE OF INVENTION: Gibberellin 2-Oxidase

FILE REFERENCE: 0623.0970000

CURRENT FILING DATE: 2003-09-26

PRIOR PILING DATE: 2000-12-08

PRIOR PILING DATE: 1999-06-11

PRIOR PILING DATE: 1999-06-11

PRIOR PILING DATE: 1999-06-11

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1998-07-15

NUMBER OF SECIL DATE: 1998-07-15
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US-10-670-454-9
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Fublication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Rovalic David K

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Uncleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Uncleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Uncleic Acid Molecules Associated With

TITLE OF INVENTION: Soy Uncleic Acid Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53223) B

CURRENT APPLICATION NUMBER: US/10/424, 599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 21951
                                                                   959 TACTTTGGAGGTCCACCATTGAGTGAAAATAGTACCATTATCTTCACTTATG---AAA 1015
                                                                                                                                   GGAGAGGAGTGTTTGTACAAAGAGTTCACATGGTGTAAATACAAGAAGGCTGCGTACACT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AACAACAAGAAAATGGTGTTGCTGTCCAAAGCAACAACAGAACAATACTCCTACATCAA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 ACCATTCAAGTCCACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GAACTACATGCCAACTGCATTCTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 TGGTGTTCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAA 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 TGGTGTCCCCAFTGAAGCTATATCCCAATTGGAATATGAAGCCTTCAAACTTCTTCTTCTA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 ATCTCAGTCCGAGAAAGACAGAGCTGGTCCCCCGACCCTTTCGGCTATGGTAGCAAGAG 354

    TGCCACTCAATGAGAAAAAAGTAGGACCTCCCAATCCATTTGTTGGGTGTAGCAAGAA 459

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415 TGTTATCTCACCCAAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGT 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               572 GTTGAACAGTTACATGTCTTCTGTGAGGAAGATGGCATGTGAGATTCTTGAGGTTGATGGC 631
                                                                                                                                                                                  1016 GGAAAAGAAAGCTTATACAAAGAGTTTACGTGGGTTCGAGTATAAAATTTAACCTATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 AACAACAACAACCATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAA
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Pred. No. 4.7e-105;
0; Mismatches 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119826C.1
US-10-424-599-21951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.2%;
Best Local Similarity 64.2%;
Matches 650; Conservative
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US-10-424-599-21951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTCGGTTGGGTCGAATACCTCCTCCAACACCCAACCCTGATGTTATCTCACCCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495 AACCGAGGAACACATTAGCAAGCTTGTGTCTGACCAAAACACGGACTCGATATTGAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.1%; Score 356.6; DB 8; Length 63.2%; Pred. No. 4.7e-93; ive 0; Mismatches 329; Indels
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: PCT/GB99/01857
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PRIOR APPLICATION NUMBER: GB 9812621.8
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 5
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// LOCATION: (1243, 1265)

// OTHER INNERWATION: unidentified residue

US-10-670-454-5
                                                                                                                                                                                                                                                                                                       LENGTH: 1318
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Matches 586; Conservative
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Publication No. US20040229357A1
GENERAL INFORMATION:
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT FILING DATE: 2003-09-26
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VS-10-437-963-78659

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Sequence 78659, Application US/10437963

Sequence 78659, Application US/2040123343A1

Sequence 78659, Application NO. US20040123343A1

Sequence 78659, Application NO. US20040123343A1

SERVICANT: La Rosa, Thomas J.

APPLICANT: Explain Tou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLI
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US-10-437-963-78659
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APPLICANT: Kayano, Tobbilaki
APPLICANT: Kobayashi, Masatomo
APPLICANT: Acbayashi, Masatomo
APPLICANT: Sakamoto, Tomoaki
APPLICANT: Sakamoto, Tomoaki
APPLICANT: Sakai, Miho
ITLE OF INVENTYO: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT APPLICATION NUMBER: US/2003-03-18
NUMBER OF SEQ ID NOS: 7
PRIOR APPLICATION NUMBER: JP 2002-276051
PRIOR PRIING DATE: 2002-09-20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 984
                                                                                                                                                                                                                                                                                                         963 GTTTGTACAAAGAGTTCACATGGTGTAAATACAAGAAGGCTGCGTACACTTCAAGGCTAG 1022
69 TGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCCA 128
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Publication No. US20040060080A1
GENERAL INFORMATION:
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al Similarity 60.9%;
598; Conservative (
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OTHER INFORMATION:
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Best Local Similarity
Matches 598; Conserv
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LOCATION: (1)
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APPLICANT: La Rosa;
APPLICANT: La Rosa; Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 65575
LENGTH: 1611
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Pred. No. 4.8e-81;
0; Mismatches 397; Indels
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US-10-425-115-69575
                                      US-10-425-115-69575
; Sequence 69575, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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58.9%;
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586; Conservative
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ORGANISM: Zea mays
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Best Local S
Matches 586
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956 GAGGAGTGTTTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCA 1015
                                                                                                    1000 TTCGCGGGGCCGCCGCTGGGGGAGCGAATCGCCGCTGCCGCAGGTGCTGGCGGAGGGA 1059
                                                                                                                                         1060 GAGGAGACCTGTACAAGGAGTTCACGTGGGGCGAGTACAAGAAGGCCGCGTACAAGACG 1119
                                                     896 TTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGA 955
820 ACCTCCGGCCTGCAGATCGCGCTCCGCGACGGCGCGCAGTGGGTCTCCGTGCCCTCCGAC 879
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Search completed: December 28, 2005, 01:23:05 Job time : 1242.83 secs

## November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions .rnpbm (Published\_Applications\_NA\_Main) and .rnpbm (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_Main) and .rapbm (Published\_Applications\_AA\_New).

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Result
No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Agred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                   Score
                                               56.4
40.8
40.6
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seq length: 2000000000
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1: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

2: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US10 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US10 NEW PUB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US11 NEW PUB.seq:*

8: /cgn2 6/ptodata/2/pubpna/US11 NEW PUB.seq:*

9: /cgn2 6/ptodata/2/pubpna/US11 NEW PUB.seq:*

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Match Length
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Gapop 10.0 , Gapext 1.0
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1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyright
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                  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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7 US-11-152-892-5

0 US-10-750-185-48573

7 US-11-152-892-3

1 US-11-152-892-2

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1 US-11-112-908-44

1 US-11-112-908-45

6 US-10-995-561-13312

6 US-10-995-561-13312

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6 US-10-995-561-52521

6 US-10-750-185-64795

6 US-10-750-185-53362

US-11-121-086-46

6 US-10-750-185-59293

6 US-10-750-185-796

6 US-10-995-561-13293

7 US-11-121-086-52

6 US-10-750-185-31828

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6 US-11-152-892-1

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Sequence 5, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 3, Appli
Sequence 13286, Appli
Sequence 13286, Appli
Sequence 1312, A
Sequence 1312, A
Sequence 1, Appl
Sequence 1, Appl
Sequence 52521, A
Sequence 52521, A
Sequence 52521, A
Sequence 52521, A
Sequence 53362, A
Sequence 5362, Appl
Sequence 5362, Appl
Sequence 5362, Appl
Sequence 131828, A
Sequence 1328, A
Sequence 1, Appl
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2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.6	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	2.7	4.1
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US-10-793-626-4305	US-10-955-054A-103	US-11-121-086-15	US-10-750-185-28226	US-10-821-234-73	US-11-121-086-55	US-11-121-086-72	US-11-117-187-211	US-10-750-185-34028	US-11-174-166-19	US-10-750-185-54120	US-10-995-561-13503	US-10-750-185-42377	US-10-750-185-47560	US-10-750-185-48102	US-11-157-389-2	US-10-927-641-127	US-10-750-185-57430	US-11-117-187-212	US-10-995-561-13278	US-10-750-185-37195	10-171-171-004
Sequence		Sequence	Sequence	Sequence	Sequence	Sequence 72, Appl	Sequence	Sequence	Sequence	Sequence	Sequence 13503, A	Sequence	Sequence	Sequence	Seguence	Sequence 127, App	Sequence	Sequence	Sequence	Sequence 37195, A	octuerre
4305, Ap	103, App	15, Appl	28226, A	73, Appl	55, Appl	72, Appl	Sequence 211, App	34028, A	19, Appl	54120, A	13503, A	42377, A	47560, A	48102, A	2, Appli	127, App	57430, A	212, App	13278, A	37195, A	TOUR 'ED

## ALIGNMENTS

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Sequence 5, Application US/11152892

Publication No. US20050251883A1

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Schomburg, Fritz M.

APPLICANT: Schomburg, Fritz M.

APPLICANT: Michaels, Scott D.

APPLICANT: Bizzell, Colleen M.

TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants

FILE REFERENCE: 960296.97605

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION STATES CONTROL OF THE CONTROL
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US-11-152-892-5
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PRIOR FILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.3%; Score 56.4; DB 7; Best Local Similarity 55.7%; Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORCANISM: Arabidopsis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1014)
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                                                                                                                                                                                                                                                                                                                                                                                 764
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                                                                                           ATATAGCACCTTTA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGG 860
TTATAGAGTGTTCA
                                                                                                                                                                                                                                                                                 СТGАСАСААСGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAA 920
                                                                                                                                                                                                                                                                                                                                                                                 GTGACTTATTTCAGGCATGGAGCAATGGCATGTACAAAAGTGTTGAACACCGTGTGATGA
                                                                                                                                                                                           CGAACCCAAAGGTGGAGAGATTCTCAACGGCTTATTTTATGTGTCCATCATACGACGCCG
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897
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883

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US-11-121-086-71

Sequence 71, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

APPLICANT: NIELSEN, KIRSTEN V.

APPLICANT: NIELSEN, KIRSTEN V.

FITTLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE REFERENCE: 09138.6000-00000

CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-05
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US-10-750-185-48573/c
                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-71
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CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 48573
LENGTH: 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48573, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
                                                                                                                                                                                                                                        SEQ ID NO 71
LENGTH: 164527
                                                                                      Matches
                                                                                                           Query Match
Best Local :
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APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMILION-2
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/567,570 PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Bovine 19866880619350
149090 TGCTTAATAAAATGTAACAGTAACTTTTTGCTATCTTTAAGAAGTGGGATTATAGGTGATT 149149
                                      1060 TGATTAACCAAACACACCCTTCAAATTCCACTCATTTTACGCACGTGTTATTACCCCAAT 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1166 TGACTCTACTTGACATATATAGAAAATGAATAGGTTAAGATGTTTATCATTT 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
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Similarity 52.0%;
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ROSENFELD, David
HOLM, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACGCAAATCTGGTTACTTTCATAATTATGACATCACTATGTTCAAGATTT 1127
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                                                                                      Conservative
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52.3%; Pred. No. 0.
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                                                                                 Score 40.6; DB 7;
Pred. No. 2.4;
0; Mismatches 84;
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                                                                                                                             Length 164527;
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APPLICANT: Amasino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Mizzell, Colleen M.
FILE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/10/155,435
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/11152892 Publication No. US20050251883A1 GENERAL INFORMATION:
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Matches
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Best Local &
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APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Bizzell, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
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NUMBER OF SEQ ID NOS: 12
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LOCATION: (1)
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ORGANISM: Arabidopsis
                      TYPE: DNA
                                          LENGTH: 3861
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Pred. No. 0.17;
0; Mismatches
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ORGANISM: Homo sapiens
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1):..(1125000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-995-561-13286
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US-10-995-561-13286
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                                                                                                                                     US-11-112-908-44/c
Sequence 44, Application US/11112908
Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer B
FILE REFERENCE: 04-164-US
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SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 13.286
LENGTH: 1125000
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Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
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Best Docal Similarity
Matches 95; Conservat
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
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Pred. No. 19;
0; Mismatches
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Pred. No. 0.65;
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PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 44
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Publication No. US20050260659A1
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
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PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 511
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PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-11-30
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CURRENT FILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-04-23
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CURRENT FILING DATE: 2005-04-22
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  TYPE: DNA
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64972 GATTTAGGAGTAATGATGATGATGATATACAATTTTTATTTTATTTTATTTTA 64919
                                                                            65032 ACAAAATAAAGCAAAGAGTGTTAGTTGATACAAAATAATCAACATTTTACAGTATGGAT
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                                                                                                                  836 AAAAGTGTAAAGCATAGGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTAC
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                               TTTGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTA 949
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                                                                                                                                                           Score 38.8; DB Pred. No. 8.5; 0; Mismatches
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US-10-995-561-13312
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SOFTWARE: FRAESEQ for Windows Version 4.0
SEQ ID NO 13312
LENGTH: 130472
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13312, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, MICHELE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1
LENGTH: 1258
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/10997437A Publication No. US20050250184A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Peptide Hormones Zalpha48 and FILE REFERENCE: 03-16 CURRENT APPLICATION NUMBER: US/10/997,437A CURRENT FILING DATE: 2004-11-24 PRIOR APPLICATION NUMBER: 60/525,597 PRIOR FILING DATE: 2003-11-26 NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10-997-437A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sheppard, Paul O. APPLICANT: Fox, Brian A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: CL001559
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Local Similarity 50.6%;
nes 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 2.9%;
Local Similarity 51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59952
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                                                                                                                                                       1203 AGATGTTTATCATTTTCTTTTTTCTTTGTTTCATCTAAGTGTAACAGTTGGTCTCAACTTCC 1262
                                                                                                                                                                                                                                                                                                              1143 TGTCTGTCTAGGTTTCAAACAGTTGACTCTACTTGACATATATAGAAAATGAATAGGTTA 1202
                                                                                                                                                                                                                                                                                                                                                                                                90;
ATCTGTGGCTAATTCTGTTGGTCGTTTGTATTATAAATGTAAAATAGTATTCCAGCTATT 1191
                                                                                                                                                                                                                                     TATTTGGAACGGCATGAAAATTAAAATTTCGGTCATGTTTTAGAGACAGTGGAGTGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38.4; DB 6; Length 1258; Pred. No. 0.57;
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Pred. No. 8;
0; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                86; Indels
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Sequence 52521, Application US/10995561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONTITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

TYPE: DNA
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US-10-750-185-64795/c
; Sequence 64795, Application US/10750185
; Publication No. US20050260603A1
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US-10-995-561-52521
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; ORGANISM: Bovine
US-10-750-185-64795
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                                                                                                                              ; ORGANISM: Homo sapiens 
US-10-995-561-52521
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                                                                         Query Match
Best Local Similarity
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Best Local Similarity
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SEQ ID NO 64795
LENGTH: 4873
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APPLICANT: MMI GENOMICS, INC.
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 64922
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1118 ATTITCTTTCCTTTTTCCTGTGTCTGTGTCTAGGTTTCAAACAGTTGACTCTACTTG 1177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BATES, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROSENFELD, David HOLM, Tom
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                                                          Conservative
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                                                                         2.8%;
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Pred. No. 2.5;
                                                        Score 37.2; DB Pred. No. 0.42; 0; Mismatches
                                                                                        DB 6;
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                                                                                                                                                                                                                                                                                                                          DRUG RESPONSE, METHODS
                                                                                          Length 201;
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David

Levicant Bates, Stephen

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM11100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 53362
LENGTH: 2555
TYPE: DNA
ORGANIS**
                                                                                              US-11-121-086-46

Sequence 46, Application US/11121086

Sequence 46, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: PUBLISEN, KIRGTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR TILING DATE: 2004-05-04
PRIOR TILING DATE: 2004-05-04
PRIOR TILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
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Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
                                                    SEQ ID NO 46
LENGTH: 158410
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Best Local Similarity
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CT 1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTTAACATGCACCTTCTATACTTTTTCTTTACACTTTGCTGCCTAGATTTCCTCCAA
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Pred. No. 1
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PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 59293
LENGTH: 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No. US20050260603A1
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Best Local
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CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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TTATCTCA 367
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Search completed: December 28, 2005, 01:30:10 Job time: 242.513 secs

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AB181373 Vigna ang
AB031206 Lactuca B
AR452812 Sequence
AR528430 Sequence
AR528430 Sequence
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AF100395 Pisum sat
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AF101382 Pisum sat
AF101382 Pisum sat
AF101382 Pisum sat
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AJ132437 Arabidops
AB067639 Daucus ca
AR452818 Sequence
BT009225 Triticum
BT002763 Arabidops
AR452818 Sequence
BT003763 Arabidops
AR452818 Sequence
BT003763 Arabidops
AX44594 Sequence
AX085539 Arabidops
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AX132435 Arabidops
AX132435 Arabidops
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosida; eurosida I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
Phaseolus.
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AR44995 Sequence
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BT002987 Arabidops
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Dna constructs and methods to enhance the production
commercially viable transgenic plants

Patent: WO 2004092390-A 3 28-OCT-2004;

Monsanto Technology LLC (US)

Location/Qualifiers
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Larity 100.0%; Pred. No. 2.1e-291;
Conservative 0; Mismatches 0; Indels
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BT009225
BT002763
AY085539
ATH132435
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AR528430
AB125233
AF056935
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BD243009 Enzyme. 7
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AB181372 Vigna ang
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AY58820 Nerium ol
AY594292 Nerium ol
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AJ302041 Cucurbita
AB125232 Nicotiana
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L Patent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL
OS Phaseolus coccineus (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-1998 JP 200554838
PR 11-JUN-1999 GB 981281.8 J5-JUL-1998 GB 9815404.0 PI STEPHEN GREGORY THOWAS, PETER HEDDEN, ANDREW LEONARD PHILLIPS PC C12N15/04, A01H5/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10, PC C12N15/09, C12N15/00, C12N15/0

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Location/Qualifiers
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                                                                                                                              AAAGACAGAGGTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAAGATTGGCCCAAAC
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/ train lation="MYVLSQPALNQPPLLKPPKSTPLFTGIPVVDLTHPDAKNLIVNA CRDFGFFKLVNHGVPLELMANLENBALRFFKKSQSEKDRAGPPDPFGYGSKRIGPNG VGWYZYLLLMYNPDVISPKSCFRLHYPRVBYYITAKOMCYAVLELMAEGLG IRQRWILSRLLKDEKSCFRLHYPPPCPEVQALNPRUVGFGEHTDPQIISVLENSST SGLQICLTDGTWYSVPPDQYSPFINVGDALQWMTNGRFKSVKHRVLADTTKSRLLSNIF FGGFALSSIY FGGFALSENIYFKSFTWCEYKKAVAYTSRLADTTKSRLLSNIF
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Molecular cloning and functional expression of gibberellin oxidases, multifunctional enzymes involved in gibberellin deactivation
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Phillips, A.L.
Direct Submission
Submitted (18-JAN-1999) Phillips A.L., Plant Sciences,
Ashton Research Station, Long Ashton Research Station,
BS41 9AF, UK
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2-oxidase, gene ga2ox1.
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llarity 100.0%; Pred. No. 2.2e-291;
Conservative 0; Mismatches 0;
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/dev stage="Late developing seeds"
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/protein id="CAB41036.1"
/db_xref="G1.4678586"
/db_xref="G03.09X083"
/db_xref="UnliProt/TrEMBL:09XG83"
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/organism="Phaseolus co
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100.0%; Score 996; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.2e-291;
Matches 996; Conservative 0; Mismatches 0;
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CRDYGFFKLVNHGVPLELVANLENBALRFFKKSQSEKDRAGPPDFGVGSKGIGPNGD
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FGGPALSEKIAPLPSVWVKGEESLYKEFTWWEYKKAAYTSRLADNRLAPFEKSATD"
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Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture, 1-1-1 Yayoi, Bunkyo, Tokyo, 113-8657, Japan (E-mail:nkjm@pgrl.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192, Fax:81-3-5841-8025)
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.larity 95.3%; Pred. No. 1.8e-268;
Conservative 0; Mismatches 47; Indels 0;
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/clone="varanism="line"

/db xref="taxon:3914"

/clone="varanism="line"

/country="Japan"
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83. .1081
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2 (bases 1 to 1360)
Nakajima,M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I. Burct Submission
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Vigna angularis VaGA2oxA1 mRNA for gibberellin 2-oxidase, complete
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   AAAGACAGAGCTGGTCCCCCCGGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC
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OY 601 TTTGGGGAGCACACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660  Bb 683 TTTGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC 660  684 TTTGGGAACTCTCACAGACCCACAGATAATTTCTGTCTTAAGATCTAATAGCACATCAGGC 742  OY 661 TTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTT 720  T13 TTGCAAATCTGTCTGCAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTT 802  OY 721 TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG 862  Bb 803 TTCATCAATGTTGGTGATGCTCAACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG 862	Qy         781 CATAGGGTTTTGGCTGACACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA 840           Db         863 CATAGGGTTTTGGCTGACACGAAGTCAAGGTTATCAATGATATCATTGGAGGACCA 922           Qy         841 GCGTTGAGTGAAAATAAGCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGTGTTTG 900           Db         923 GCGCTGAGTGAAAAAAAGAAGACCCTTTACCTTCAGTGATGGTAAAAGAGAGAAAGATTG 982           Qy         901 TACAAAGAGTTCACATGGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960           Qy         1 TACAAAGAGTTCACATGGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960	983 961 043 1 See 1	VERSION AR528429 VERSION AR528429 VERSION AR528429.1 GI:53916494 KEYWORDS SOURCE Unknown. Unclassified. Unclassifi	Query Match         83.1%; Score 827.4; DB 6; Length 1359;           Best Local Similarity 89.9%; Pred. No. 4:9e-240;         A1.5e-240;           Matches 898; Conservative 1; Mismatches 97; Indels 3; Gaps 1;           Db         102 ATGGTTGTTCTGTCTCAGCCAGCATTATACCAGTTTTTCCTTCTGAAACCATTCAAGCC 60           Cl

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Unpublished
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2 (bases I to 1245)
Direct Submission
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular
Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular
Ge Plantas, Consejo Superior de Investigaciones Científicas (CSIC),
Universidad Politecnica de Valencia, Avda. de los Naranjos s/n,
Valencia 46022, Spain
Location/Qualifiers
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IQPKKVPEXLLMDEQSDVPRLINIYPEP PDLOLEHGRNLIGFGBHTDGOQTISVLASNN
TSGLQIQLKDGSWISIPPDQSSFFINVGDSTQVLTNRFKSVKHRVLANSMKSRLSMI
YFGGPPLSRKIAPLPSLMEGEBOSLYKETWFFYKKSAVKSRLADNRLVLFEKIAAS"
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/product="GA_2-oxidase_2"
/protein_id="AAT92094.1"
/db_xref="GI:51011366"
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/db_xref="taxon:63479"
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KACQEFGFFKVINHGVPLEFTTKLEGBAVKFFNLPQPEKEKTRPAKFPGYGNKRIGGN
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KIGPRNVLSKLLANTNPELAYEKAVTIPGDSELFWSCVNDYVSAVRSMACDVLDMTADGL
KIGPRNVLSKLLENDSDAVFRLANTPPGDSELFMSCKRILIGFGFTDPQIISUKDCTWVSVPPDQYSFFINNGDSLQVMTNGFRSVKHRVFDADGLKSRVSM
IYLGGPPLDEKIAPLSSLMEEGEESLYKEFTWCEYKKSAYKTRLGDNRLKFFEKSVGQ
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Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas, CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn, Valencia 46022, Spain Location/Qualifiers
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Pred. No. 2.1e-135;
0; Mismatches 266; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                 product="gibberellin 2 oxidase"
protein id="AAT72916.1"
db_xref="G1:50293061"
                                                                                                                                                                                                                                                                                                       /gene="GA2ox3"
/note="GA 2-oxidase; NoGA2ox3"
                                                                                                                                      /organism≂"Nerium oleander"
                                                                                                                                                                                             f="taxon:63479"
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                                                                                                  Frisse, A. and Lange, T. Gibberellin biosynthesis in young seedlings of Cucurbita maxima Unpublished
 gene; gibberellin 2-oxidase
 ga2Ox gene; gibberellin 2-oxidas
Cucurbita maxima (winter squash)
Cucurbita maxima
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/function="2-oxoglutarate dependent dioxygenase"
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1. Similarity 69.0%; Pred. No. 1.6e-128;
647; Conservative 0; Mismatches 288; Indels 3;
Direct Submission
Submitted (19-70N-2001) Lange T., Botanical Institute,
Braunschweig, Mendelssohnstr. 4, D-38106 Braunschweig,
related entry AJ315662.
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/mol_type="mRNA"
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/db_xref="taxon:3661"
/dlone="2beta="W82"
/tissue_type="root tips"
/dev_stage="7 day old seedling"
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/db_xref="GI:32127337"
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/organism="Cucurbita
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Best Local Si
Matches 645
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Submitted (14-DBC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelssohnstr. 4,
Braunschweig, D-38106, GERMANY
Location/Qualifiers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene)
AJ302041.1 GI:27123664
ga2Ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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developing seeds of Cucurbita maxima L
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| /organism="Cucurbita maxima" |
| /organism="Cucurbita maxima" |
| /orlivar="Riesenmelone, gelb gen |
| /db_xref="taxon:3661" |
| /clone="2beta-EMBRYO" |
| /dev_stage="developing embryos" |
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195 ATTGTTAAGGCCTGTGAAGAATTTGGATTCTTCAAAGTCATTAACCATAGCGTCCCTACG 254  181 GAGTTAATGGCCAATTTAGAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGGG 240  255 GAATTCATAACTAAACTTGAATCTGAAGCCATCAAATTCTTCTCCTCTCCCCTTTCTGAG 314  241 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAACTAGGTAGCCCAAAC 300  315 AAACAAAAGCTGGGCCGACCCTTTTGGCTATGGTAGCAAGAACTAGTACTCACCCAAT 374  301 GGTGATGTCGGTTGGGTCGAATACCTCTCCTCCACACCTGATTATCTCACCC 360		555 541 615 598 675 675 735		MRY09113 MMY09113 MMY09113 ACCESSION ACCESSION Y09113 WERSION Y09113.1 GI:1666095 Gioxygenase. Gioxygenase. ACCESSION Y09113.1 GI:1666095 Gioxygenase. Marah macrocarpus ORGANISM Marah macrocarpus Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Marah. REFERENCE AUTHORS MacMillan,J., Ward,D.A., Phillips,A.L., Sanchez-Beltran,M.J.,
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	AB125232 LOCUS DEPINITION Nicotiana tabacum GA2ox1 mRNA for gibberellin 2-oxidase 1, complete cds. ACCESSION AB125232 VERSION AB12523.1 GI:46849528 KEYWORDS Nicotiana tabacum (common tobacco) OKGANISM Nicotiana tabacum ORGANISM Nicotiana tabacum Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Oyre eudicotyledons;	គល ។គល ។	FEATURES LOCATION) Qualifiers    1.1292	ORIGIN  Query Match Best Local Similarity 66.7%; Score 443; DB 15; Length 1292; Best Local Similarity 66.7%; Pred. No. 5.5e-123; Matches 664; Conservative 0; Mismatches 325; Indels 6; Gaps 2;  Qy 1 ATGGTGTCTGTCTCGCGCATTGACCAGTTTTCCTTCTGAAACCATCAAGTCC 60  Db 75 ATGGTGTCTTAACTAAACCTGGCATTTCCCCATAGTCAAAAACTGCAAATTA 134  Qy 61 AGGCCCTTGTTCACGGGATTCTTGTGGTCGACCTCAGGACCTCAGAGAATTC 120  Db 135 TCCTCATTCTCAGGGATTCCTGATGGTCGTCCTTCAAACCTAAAACTTAAAACTT 194  Qy 121 ATAGTGAACGCCTGTAGGTGTTCATGATGATCATCTAAAACTTAAAACTTTAAAACCTTTAAGAACCTT 194  Qy 121 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTTGAACCTTAAAACCTTAAGAACCTT 194

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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons;
rosids, eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 1350 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations A
                                                                                                                                                                                                                                                                                                                                                                  TGGAGGACCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGA
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                  TTTGGTTGGGTTTGGGGAGCACACACACACACACAGATAATTTCTGTCTTAAGATCTAACAG
                                              CATGATTGGATTTGGAGAACACAGACCCACAGATCATTTCGGTTTTGAGATCTAATAA
                                                                                                                         CACATCTGGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCA
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    .1026
    Organisma="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

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KVINHGVPMEFISTLESESTKFFSLPLSEKQRAGPPSPFGYGNKQIGRNGDVGWVZYL
Gaskin, P., Lange, T. and Hedden, P.
Gibberellin biosynthesis from gibberellin A12-aldehyde in endosperm
and embryos of Marah macrocarpus
plant Physiol. 113 (4), 1369-1377 (1997)
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MGESESDSVERYNHYE PRCPEELQALESTRMI GROSHTDRQI I SVLRSNNYFGGLQI SLLPD
MMI SVPPDQTSPFINYGDSL, GVOWTNORFKSVKHRVLINSLKSRI ISVLRSNI Y FGGPPLSEK
I APLISSLMKGEBESLYKKETWFEXKRSARVSKILANNRLVHFERI AAS."
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                                                                                                                                                                             Direct Submission
Submitted (31-OCT-1996) P. Hedden, University of Bristol,
Department of Agricultural Sciences, IACR-Long Ashton Research
Station, Long Ashton, Bristol, BS18 9AF, UK
Location/Qualifiers
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Pred. No. 7.6e-121;
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/dev_stage="immature seed"
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/clone="M7-3"
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Matches 656; Conservative
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                                                               GAATACCTCCTCCAACACCCAACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC
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Adm94203 Rice Diox Adm94201 Corn Diox Aaz99474 Cotton gi Adx1608 Plant ful Adx15208 Plant ful Adx09682 Plant ful Adx09682 Plant ful Adx09812 Rice gene Adx69586 Plant ful Adx09478 Maize gib Adx09478 Maize gib Adx09478 Corn isop Adx09473 Soybean g Adx040268 Arabidops Adx09475 Cotton gi Adx040259 Arabidops Adx05021 Arabidops Adx053074 Arabidops Adx053074 Arabidops Adx053074 Arabidops Adx053074 Arabidops Adx053074 Arabidops Adx0557 Maize gib Adx0267 Maize GA

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DNA plasmid; transfer DNA; T-DNA; Agrobacterium Ti plasmid; transgene; expression cassette; transgenic plant; transgenic; plant; gibberellin 2-oxidase; ds.
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AAD40264
ADX11608
AD145210
ADX13286
ADX09682
                                                                                                                                                                   ADX63586
AAZ99478
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AAD40263
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Phaseolus coccineus.
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Aaz9471 Soybean g
Aad40261 Soybean G
Ab213545 Arabidops
Ad67975 Arabidops
Ad25916 Arabidops
Ad35916 Soybean D
Ad994205 Soybean g
Ad44026 Soybean g
Ad44026 Soybean g
Ad42027 Arabidops
Adm94207 Wheat Dio
Aaz55917 Arabidops
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996
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Listing first 45 summaries
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ALIGNMENTS

New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid first border region linked to a transgene linked to an Agrobacterium Ti plasmid second border region, useful for enhancing production of The present invention relates to a DNA plasmid comprising a transfer DNA (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked to at least one transgene linked to an Agrobacterium Ti plasmid second border region, and located in the DNA plasmid outside of the T-DNA is a plant expression cassette comprising a plant cell non-lethal negative Example 1; SEQ ID NO 3; 77pp; English. WPI; 2004-758349/74. transgenic plants.

AAZ59472 AAD40262 AAZ55917 ADM94207 AAC39277 AAZ5915 AEB67733 ADA70120 ADK00081

8 12 14

ADM94213 ADM94205

12 2

Ye X;

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selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter is a constitutive promoter. The promoter expresses the linked non-lethal negative selection marker gene product in tissue culture during plant regeneration. The plant cell non-lethal negative selectable marker gene comprises a plant hormone biosynthetic pathway gene, degradative gene, biosynthetic pathway gene or signalling gene, or metabolic interference biosynthetic pathway gene or signalling gene, or metabolic interference from antibiotic resistance and herbicide resistance. The transgene comprises a transgene of agronomic interest. The plant hormone comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway genes, and abscisic acid pathway genes. The plasmid is useful for enes, cytokinin pathway genes, auxin pathway gene, ethylene pathway genes, and abscisic acid pathway genes. The plasmid is useful for enhancing the production of commercially viable transgenic plants. The present sequence representes bNA encoding Phaseolus coccineus gibberellin production of commercially viable transgenic gibberellin production of commercially by selected the production of commercially viable transgenic gibberellin production of commercially viable transgenic gibberellin production of commercially viable transgenic gibberellin production of commercially by an operative selected the production of commerc
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Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                  ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC
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                                                                                                1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
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             Length 999;
                                                          Indels
Louery match
Best Local Similarity 100.0%; Score 996; DB 13;
Matches 996; Conservative 0; Miamatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-oxidase, PcGA2ox1. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in
                                                              TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG
                                                                                                                GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTG
                                                                                                                                                                                                                     841 GCGTTGAGTGAAAATATAGGACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGGAGTGTTTG
                                                                                                  CATAGGGTTTTGGCTGACACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibberellin 2-oxidase; PcGA2ox1; runner bean; 2-beta-hydroxylation; inactivation; growth inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68. .1066
/*tag= a /product= "Gibberellin 2-oxidase PcGA2ox1"
/product= "Gibberellin 2-oxidase PcGA2ox1"
/transl_except= {pos:1058. .1063, aa:Ala}
                                                                                                                                                                                                                                                        966
                                                                                                                                                                                                                                                                      AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT 996
                                                                                                                                                                                                                                                                                                                                                                                                                         Runner bean gibberellin 2-oxidase PcGA2ox1 cDNA
                                                                                                                                                                                                                                                       961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                AAZ55912 standard; cDNA; 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-GB001857,
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                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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P-PSDB; AAY58597.
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15-JUL-1998;
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tissues. The mucleic acids can be used to transform plants so that tissues. The mucleic acids can be used to transform plants so that cardiace the concentration of bioactive glas in the plants and the concentration of bioactive glas in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing lodging-cesistance and grain yield in cereals, improving seedling quality, reducing the growth of amenity grasses, reducing shoot growth in orchard and orneasing yields for the diversion of assimilates from vegetative to conditional processing by the growth of amenity grasses, reducing shoot growth in orchard and increasing yields (by the diversion of assimilates from vegetative to creproductive organs). The nucleic acids may also be used to induce male and increasing plants, inhibit creversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic growth in seedless grass, increase stem length and therefore and growth in seedless grass, increase stem length and therefore texture and fruit shape in apples, increase stem length and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species.
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     ensuring that the active hormones do not accumulate in plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 996; DB 3; Length 1
100.0%; Pred. No. 6.7e-310;
ive 0; Mismatches 0; Indels
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Matches 996; Conservative
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                                                                                                                                                                       ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG
                                                                                                                                                       AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC
                                                                                                                                                                                                                  GGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCC
                                                                                                                                                                                                                                    GGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCAACCCTGATGTTATCTCACCC
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                                                                                          GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
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TTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTTAAAAGTGTAAAG
                                                             Treatcargetregregecerteracagerargacraategeagerrraaaagreraaag
                                                                                                                  CATAGGGTTTTGGCTGACACGAAGGAAGGTTATCAATGATGATCTACTTTGGAGGACCA
                                                                                                                                           GCGTTGAGTGAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTG
                                                                                                                                                                      GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGGGTGTTTG
                                                                                                                                                                                                TACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT
                                                                                         CATAGGGTTTTGGCTGACACGAACGAAGGTTATCAATGATCTACTTTGGAGGACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Obtaining transgenic plant useful for controlling seed germination ar seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a gibberellic acid 2-oxidase 1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "gibberellic acid 2-oxidase 1" /trans except= (pos: 633. .635, aa: Xaa) /note= "Xaa is an unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heck GR, Kishore GM, Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean gibberellic acid 2-oxidase 1 cDNA sequence.
                                                                                                                                                                                                                                                                  1028 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCTGAT 1063
                                                                                                                                                                                                                                                    AATAGGCTTGCCCCTTTCCAGAAATCTGCTGAT 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
102. .1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 45; Page 248; 267pp; English
                                                                                                                                                                                                                                                                                                                                                ВЪ
                                                                                                                                                                                                                                                                                                                                                AAZ99471 standard; cDNA; 1359
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P-PSDB; AAY84099.
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07-JUN-1999;
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778 AAGCATAGGGTTTTGGCTGACACCAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGA

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The specification
                  describes methods for the inhibition and control of gibberellic acid a chiefle. Gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin blosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, oxidase, phytoene synthase, C20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1359;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
sequence, which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 827.4; DB 3;
Pred. No. 1.7e-255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              83.1%;
89.9%;
                                                                                                                                                                                                                                                                                                                                          compared to normal plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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777 360 420 480 540 597 717 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180 ATAGTCAATGCCTGCAGGACTTCGGCTTCTTCAAGCTCGTGAACCACGCTGTTCCGTTA 281 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAÇ 300 461 581 641 701 657 761 821 102 ATGGTTGTTCTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAGCCC 161 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120 162 ACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACCCAA 341 AAAGACAGGGCTGGTCCCCCTGACCCTTTTGGCTACGGCAGCAAGAGGATTGGCCCTAAC 401 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAATTTTCAGGGCGGTGGTGGAGGAATAC 521 ATTAGAGCGGTGAAGAACATGTGCTATGAGTGTTGGAATTGATGGCTGAGGGATTGGG ATAACGCAGAAGAATGTGTTGAGTAGGTTGCTGAAGGATGAGAAGAGTGATYCTTGCTTC TITITCATCAATGITGGIGACGCTCTACAGGIAATGACTAATGGGGGGGGTTTAAAAGIGTA CAGTTCATGGCCAATTTGGAAAACGAAACCCTCGGGTTCTTCAAAAAAACCTCAATCCGAG GGTGATGTCGGTTGGGTCGAATACCTCCTCCAACACCCAACCCTGATGTTATCTCACCC Geceangrederresarracerecrecreaseaceaecerearererere **AAATCACTTTGCATTTTCCGAGAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTAC** <u>agacittaaccactaccccardccccaaccaccardcaaccaaccaaccaattriccit</u> GGCTTGCAAATCTGTCTCACAGATGGCACTTGGGTTTTCAGTCCCACCTGATCAGACTTCC ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGGG ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC AGGITGAACCACTACCCGCCTTGCCCTGAGGTGCAAGCACTGAAC---CGGAATTTGGTT GGGTTTGGGGAGCACACACACACAGATATTTCTGTCTTAAGATCTAACAGCACATCT Geccrecaaarcrercreacagarescarreserrrererereceacereaacrree 342 402 522 582 541 642 61 121 181 282 462 658 222 241 301 361 421 481 598 702 762 718

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced send garmination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agromomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
898 TTGTACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCT
                                           838 CCAGCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGATAAAAGGAGAGAGTGT
                                                           942 CCACCCTTGTGTGAAAAGATAGCACCTTTACCTTCACTCATGTTAAAAGGAGAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kishore GM, Logusch EW, Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                  Gibberellin, transgenic plant, seed germination, seedling growth, transgenic, 2-oxidase 1; enzyme, GA, soybean; gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_except= (pos:633. .635, aa:Xaa)
/note= "Xaa = any amino acid"
                                                                                                                                                                                               1062 garaaragacresecerrirsagaaarersersaar 1100
                                                                                                                                                                  958 GATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "GA 2-oxidase 1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 45; Page 92-93; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BROW/) BROWN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAE24921.
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                                                                                                                                                                                                                                                                                                                                                                                                   Gibberellin;
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Piller KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max
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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell plantacteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (BMZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 424.4; DB 6; Length 1026;
Pred. No. 1.5e-125;
0; Mismatches 291; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              information supplied to Derwent by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           NO 1350.
                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
                                          1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100
                                                                                                                                                                                                                                                                           Arabidopsis thaliana stress regulated gene SEQ ID
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                                                                                        ABZ13545 standard; DNA; 1026
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al Similarity 67.5%;
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                                                                                                                                                                                                                                                                           61 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120
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                                                                                                                                                                                                1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
etc., and is also useful in storage and transport of seeds to red
premature germination which may affect agronomic or food quality
seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
                                                                                                                                                      3;
                                                                                                                   DB 6; Length 1359;
                                                                               Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                                                                 Score 827.4; DB 6; Length
Pred. No. 1.7e-255;
1; Mismatches 97; Indels
                                                                                                               Query Match 83.1%;
Best Local Similarity 89.9%;
Matches 898; Conservative
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Goff Z.

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Glazebrook Whitham S,

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involved in plant resistance or response to pathogenic infection. Micromprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an unlinfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                  Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                 present invention relates to a method (M1) for identifying genes
                                                                                                                                                           6; SEQ ID NO 223; 899pp; English,
                      (SYGN ) SYNGENTA PARTICIPATIONS AG
22-JUN-2001; 2001WO-IB001105
                                             Chen W, Co
                                                                              WPI; 2003-175290/17
                                                                                                                                     expression
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                                           Chang H,
Katagiri
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                                  Length 1026;
Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;
                                                                     Indels
                                  Score 424.4; DB 8;
Pred. No. 1.5e-125;
0; Mismatches 291;
                                Query Match 42.6%;
Best Local Similarity 67.5%;
Matches 612; Conservative
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Plant; bacterial infection; fungal infection; viral infection; SEQ ID 223

Arabidopsis thaliana gene,

Arabidopsis thaliana

WO2003000898-A1

03-JAN-2003

(first entry)

20-NOV-2003

22-JUN-2001; 2001WO-IB001105

BP.

1026

DNA;

ADA67975 standard;

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cornulate in plant tissues. The nucleic acids can be used to transform plants so that gibberellin 2-oxidase can be constitutively over-expressed cor otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful in many agricultural and horticultural applications such as enhancing coloding-resistence and grain yield in cereals, improving seedling capality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs).

Contact prevent preverse sprouting, reduce shoot growth in hedging plants, inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and length and therefore yield in sugar cane, increase stem cleary and thubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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Pred. No. 1.6e-125;
0; Mismatches 291; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1237 BP; 356 A; 277 C; 280 G; 324 T; 0 U; 0 Other;
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Best Local Similarity 67.5%;
Matches 612; Conservative
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                                                                                                                                                                                                                                                                                                               * isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used
produce transgenic plants with improved or altered growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents cDNA encoding an Arabidopsis thaliana gibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-hydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is its only activity. Hydroxylation at the 2-beta position of a GA results in a biologically inactive product, and is the most important route for GA metabolism in plants, ensuring that the active hormones do not
                                                                                                             GCTCTTCAGGTTATGACTAACGGGAGGTTCAAGAGTGTTAAACACAGGGTCTTAGCCGAT
                                                                                                                                                                                      ACAAGGAGATCGAGGATTTCAATGATATATTTCGGCGGACCGCCATTGAGCCAGAAGATC
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            GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGAC
                                           GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAAGCATAGGGTTTTGGCTGAC
                                                                                                                                                    ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Gibberellin 2-oxidase AtGA2ox2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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98GB-00015404
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                                                                                                                                               918
ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAATATA 858
                                                                                                     ACAAGGAGATCGAGGATTTCAATGATATTTTCGGCGGACCGCCATTGAGCCAGAAGATC 975
                                                                                                                                                                                                                           TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGATAATAGGCTTGCCCCTTTC 978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EM, Miao G, Famodu OO;
Weng Z, Caimi PG, Fang Y;
Lu G, Helentjaris TG;
                                                                                                                                             GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dloxygensee; Ent-Kautene Synthase A; GA-20 oxidase; Globerellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; ABC transporter GNOX0-like; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein BPGP; P-glycoprotein HWMD2; ABC transporter; PMG TRAPGP; P-glycoprotein HWMD2; ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I, Kinney AJ, Rafalski JA, Orozco EM,
Lohman KN, Rendina AR, Sakai H, Weng
Zoughi IL, Anderson SL, Shi J, Lu G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; SEQ ID NO 13; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soybean; 88; plant; plant metabolism;
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PIONEER HI-BRED INT INC.
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99US-0143412P.
99US-0146650P.
99US-0170906P.
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CC TAIN, 4-dilipytoxyxy.2-butannon-4-phosphate synthase activity, appearing as croombinant DNA construct comprising the polynucleotide, a cell with the comprising the polynucleotide, a cell acqualatory sequence, transforming a cell with the polynucleotide, a cell comprising the recombinant DNA construct, producing a plant (comprising the recombinant DNA construct plant from the transformed plant cell), comprising transformed blant cell with the polynucleotide and regenerating a plant from the transformed plant cell), a plant comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and as eed comprising consent from GTP cyclohydrolase II/3,4-dihydroxy-2-butannone-4-phosphate CC synthase, Dioxygenase, Riboflavin specific deaminase, Ethylene response consent from GTP cyclohydrolase II/3,4-dihydroxy-2-butannone-4-phosphate CC states, Acyl-CoA thioesterase II/3,4-dihydroxy-2-butannone-4-phosphate CC states, Acyl-CoA thioesterase II/3,4-dihydroxy-2-butannone-4-phosphate CC states, Acyl-CoA thioesterase II/3,4-dihydroxy-2-butannone-4-phosphate CC stansporter and MRPA ABC transporter. PMPNO ABC transporter and MRPA ABC transporter. PMPNO ABC transporter and MRPA ABC transporter. PMPNO ABC transporter and MRPA ABC transporter. CC stansporter and MRPA ABC transporter. PMPNO ABC transporter and MRPA ABC transporter. PMPNO ABC transporter and MRPA ABC Transporter. CC stound. The polypoptides can define to receit transporter and sequence for transporter. The nucleic acid fragment may be used to probe Southern blots containing restriction endonuclease-treated genomic DNA of a set of individuals representing parent and progeny of a d
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thes 326;
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987 CCTTTGAGTGAGAAAATAGCACCATTATCCTCTCTCATG---AAAGGAAAAGAAAGTCTA 1043
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                                                                                                                                                                                                                                                          TITATTAACGITGGIGAITCTCTICAGGITATGACAAAIGGAAGGITCCGAAGIGIGAGA 926
                                                                                                                                                                                                                                                                                                                              CACAGAGTGTTGGCAAATGGGTTCAAGTCCAGGCTTTCAATGATTACTTTGGAGGTCCA
                                                                                                                                                                                                                                                                                                                                                            841 GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGGAGTGTTTG 900
                                                                                                                                                                                                                                                                                                                                                                                                                       901 TACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT 960
                                                                           CTTCAGATTTATCTTAGAGATGGAATTGGATTTCAGTCCCACCAGATGACAAATCCTTT
                                                                                                                                                 TTTGGAGAACACACACACCCACAAATCATCTCTCTTTAAGATCCAACAACACTTCAGGC
                                                         TITGGGGAGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC
                                                                                                                                                                             TTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTT
                                                                                                                                                                                                                                                                                                  CATAGGGTTTTTGGCTGACACGAAGGCTAAGGTTATCAATGATCTACTTTGGAGGACCA
481 ATAAGGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTC
                          <u> Arrcagcaaaaggargrerrragcaagcrrcraarggaraaacaaagrgacrcrarrrrc</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soybean; ss; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gabborellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; P-GIYcoproter GTN20-like; P-GIYcoprotein I; P-GIYcoprotein 3; P-GIYcoprotein APPGP; P-GIYcoprotein HVMDR2; AGC transporter; PMP70 ABC transporter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1104 AATAGACTTGAACATTTGAAAGAATTGCAGCT
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DE NEMOURS & CO E I. HI-BRED INT INC.

DU PONT I

(PION-)

99US-0143401P. 99US-0143412P. 99US-0146650P. 99US-0170906P.

12-JUL-1999; 12-JUL-1999; 30-JUL-1999;

99US-0172959P

15-DEC-1999; 21-DEC-1999; 21-DEC-1999;

2000US-00614912

12-JUL-2000;

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The invention relates to an isolated polymuclectide comprising a nuclectide sequence encoding a polypepide having GTP cyclohydrolase incledide sequence encoding a polypepide having GTP cyclohydrolase [1/34-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as a culcectide sequence, a cecombinant DNA construct comprising the polymuclectide operably linked to at least one regulatory sequence, transforming a cell with the comprising transforming a plant cell with the polymuclectide, a cell comprising the recombinant DNA construct.

The polymuclectide and regenerating a plant from the transformed plant cell), producing a plant (comprising transforming a plant cell) with the polymuclectide and regenerating a plant from the transformed plant cell), the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising che recombinant DNA construct and seed comprising che recombinant DNA construct and seed comprising chesen from GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-pholism proteins chosen from GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-pholism protein chesen from GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-pholism protein chesen from GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-pholism protein chesen from GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-pholism comprise [1/3,4-dihydroxy-2-butanone-
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                                                                                                                                                                                                       New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 GAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTTTTGTCACTCAATGAA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 Ariccircricricradaccaacaacaacaacaaracriccracarradaacriccarcca 225
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              I, Kinney AJ, Rafalski JA, Orozco EM, Miao G, Famodu OO;
Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Zoughi II, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
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Pred. No. 5.2e-124;
0; Mismatches 327;
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al Similarity 65.6%;
651; Conservative
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                                                                                                                                                             P-PSDB; ADM94206.
                   Allen SM,
Lee J, Lo
Shen JB,
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"gibberellic acid 2-oxidase 2"

/\*tag= a /product= '

WO200009722-A2

24-FEB-2000

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                                                                                                             361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTAC
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Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.

SJ;

Logusch

EW,

Logusch

Kishore GM,

GR,

Elich TD, Heck ... S. Ream JE;

SM, E

Piller

(MONS ) MONSANTO CO

07-JUN-1999;

10-AUG-1998

WPI; 2000-224351/19. P-PSDB; AAY84100.

98US-0096111P.

99WO-US018066

10-AUG-1999;

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Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta, 3beta-hydroxylase; seed germination; seedling growth; gibberallin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; se.
                                                                                               Soybean gibberellic acid 2-oxidase 2 cDNA sequence.
                        ВР
                        standard; cDNA; 1403
                                                                       (first entry)
                                                                        03-JUL-2000
                                                                                                                                                                                       EAX
                       AAZ99472
                                                 AAZ99472;
                                                                                                                                                                                    Glycine
          RESULT
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Location/Qualifiers 149. .1129

Key

361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGTGGAGAACTAC 420

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The present sequence encodes a gibberellic acid 2-oxidase 2 protein describes which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels achievels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta, 3beta-hydroxylase, 2-oxidase, phytone synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polymucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of germination, in transgenic plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n,
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                                                                                          TTTGGGGAGCACACACACACACACATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC
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The invention relates to control of gibberellin (GA) levels in plants. The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, ctc., and is also useful in storage and transport of seeds to reduce premaination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
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                                                                                                                                                                                                                           Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 ATAGTGAAGGCTTGTGAAGTTTGGATTCTTCAAAGTCATCAACCATGGTGTTCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 ATGGTGTTGCTGTCCAAGGCAACAACAACAATACTCCTACATCAAGAACTACATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGTGAACGCCTGTAGGGACTTCGGCCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 GGGGATGTTGGTTGGGTACCTTCTTCTCAACACCAATCAAGAACACACT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----referrancecaaaacecicacaaritracererererere
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   SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
       Logusch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1403 BP; 440 A; 269 C; 261 G; 433 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #2.0%; Score 418.2; DB 6; Local Similarity 66.2%; Pred. No. 1.7e-123; les 657; Conservative 0; Mismatches 318;
Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 45; Page 94-95; 155pp; English
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gibberellin (GA) 2-oxidase, PECAROXXX. This enzyme is a GA 2-beta-
bydroxylase that acts on C19-GAs and for which 2-beta-hydroxylation is
its only activity. Hydroxylation at the 2-beta position of a GA results
in a biologically inactive product, and is the most important route for
GA metabolism in plants, ensuring that the active hormones do not
accumulate in plant sensuring that the active hormones do not
accumulate in plant sensuring that the active hormones do not
accumulate in plant sensuring that the active hormones do not
cor otherwise enhanced to reduce the concentration of bioactive GAs in the
plants so that gibberellin 2-oxidase can be constitutively over-expressed
or otherwise enhanced to reduce the concentration of bioactive GAs in the
cor otherwise enhanced to inhibit plant growth. Growth inhibition is useful
in many agricultural and horticultural applications such as enhancing
lodging-resistance and grain yield in cereals, improving seedling
callity, reducing the growth of amenity grasses, reducing shoot growth in
corchard and ornamental trees, improving tolerance to cold, drought and
infection, and increasing yields (by the diversion of assimilates from
induce male and/or female sterility (by expression in floral organs),
prevent pre-harvest sprouting, reduce shoot growth in hedging plants,
inhibit reversibility in the development or germination of seeds and
inhibit reversibility and the development or germination of seeds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and pears), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase sitem celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 ATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 arccererraradacerraracedacecaardeceaaaacecaaarcereaagecarergaa 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 GAGTTTGGGTTCTTCAAAGTCATCAACCATGGGGTCCGACCCGATCTTTTGACTCAGTTG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GAGCAAGAACCATCAACTTCTTTGCTTTGCATCACTCTCTCAAAGACAAAGCGGGTCCA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 CCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 GAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCAAATCACTTTGCATTTTC 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 559 -----GAGAAGGAAGACTCCGGTCAAGGAAGAGATTGGGTTCGGTGAGCACACTGAT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC
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   sequence represents cDNA encoding an Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1008 BP; 296 A; 212 C; 232 G; 268 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 38.3%; Score 381.6; DB 3; Local Similarity 64.7%; Pred. No. 9.2e-112; Les 586; Conservative 0; Mismatches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 CCATTGAGTGAGAAAATAGTACCATTATCTTCACTTATG---AAAGGAAAAGAAAGCTTA 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  960
                                                                                                                                                                                                                                                                                                TICATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGTTGAGTGAAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGGAGTGTTTG 900
                                                                                                                                                                                                                                     crrcagarrirriciragagaricaaacrigarirricagriccaccrigarcacaarcrirc 853
                                                                                                                                                                                                                                                                                                                                        CACAGAGTTTTGACAAATGGATTTAAGTCTAGACTCTCAAATGATTTACTTTGGAGGTCCA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth
                                                                                         TITGGAGAACACAGGACCCACAAATCATITCTCTACITAGGTCCAACAATACTTCAGGC
677 AGGGTGAATCACTACCCTGCTTGCCCTGAACTT---GTGAATGGTCAAAACATGATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                   CATAGGGTTTTGGCTGACACGAAGGAGGTTATCAATGATCTACTTTGGAGGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAAAGAGTTCACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGAT
                                                                                                                                                                             TIGCAAAICIGICICACAGAIGGCACTIGGGITTCAGICCCACCIGAICAGACTICCITT
                                                          TITGGGGGGCACACAGACCCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibberellin 2-oxidase; AtGA2ox3; 2-beta-hydroxylation; inactivation; growth inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Gibberellin 2-oxidase AtGA2ox3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ55917 standard; DNA; 1008 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 9; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB001857
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98GB-00015404
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                            ,, καιαικι υΑ, Orozco ΕΜ, Miao G, Famodu ΟΟ,
Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                              ACAAAGAGGTCAAGGATATCGATGATCTACTTCGCAGGTCCTCTTTGAGCGAGAAGATT
                                                                                                                                                                           GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCATGTTGGTGAC
                                               GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAAGCATAGGGTTTTGGCTGAC
                                                                733 ACTETTEAGGTGATGACAAACGAAGATTCAAGAGTGTGAAACATAGAGTGGTGACAAAT
                                                                                   ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAAATATA
                                                                                                                                                              TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC
                                                                                                                         GCACCTTTACCTTCAGTGATGTTAAAAGGAGAGAGTGTTTGTACAAAGAGTTCACATGG
                                                                                                                                          GCACCATTATCATGCCTTGTGCCAAAGCAAGATGATTGCCTTTATAATGAGTTTACTTGG
                                                                                                                                                                                                                                                                                                                                                         GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase, Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase; Ethylene response factor; Acyl-CoA thioesterase II; Bchylene response factor; Acyl-CoA thioesterase II; P-glycoprotein ATPGP; P-glycoprotein I; P-glycoprotein 3; P-glycoprotein ATPGP; P-glycoprotein HVMDR2; ABC transporter; PMP70 ABC transporter;
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(PION-) PIONBER HI-BRED INT INC.
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99US-0146650P.
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99US-0172946P.
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P-PSDB; ADM94208.
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The invention relates to an isolated polymucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase CC In(1/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing as ADM94266. Also included are a vector comprising the polymucleotide, a callast one regulatory sequence, transforming a cell with the ccomprising transforming a cell with the producing a plant (comprising transforming a plant cell with the polymucleotide and regenerating a plant from the transformed plant cell), caplant comprising the recombinant DNA construct. Also disclosed as new are nucleic acid conversed and segementating a plant cell with the a plant comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising conversed to a plant comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct and a seed comprising conversed to a plant complyate assembled contigs encoding plant metabolism proceins chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase, bloxygenase, Ent-Kaurene Synthase A, GA-20 oxidase, Gibberellin chost proportein I, P-glycoprotein 3, P-glycoprotein ATPGP, P-glycoprotein I, P-glycoprotein By P-glycoprotein ATPGP, P-glycoprotein I, P-glycoprotein I, P-glycoprotein ATPGP, P-glycoprotein I, P-glycoprotein ATPGP, P-glycoprotein I, 
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Example 3; SEQ ID NO 7; 186pp; English.
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Theal Similarity
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9905-0139459P

9905-0139460P

9905-0139461P

9905-0139461P

9905-0139463P

9905-013963P

9905-0140693P

9905-0140693P

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9905-0141842P

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9905-014287P

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99US-0159329P.
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99US-0159638P.
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cor otherwise enhanced to reduce the concentration of bloactive GAs in the plants and therefore to inhibit plant growth. Growth inhibition is useful con many agricultural and horticultural applications such as enhancing lodging-resistance and grain yield in cereals, improving seedling capality, reducing the growth of amenity grasses, reducing shoot growth in orchard and ornamental trees, improving tolerance to cold, drought and infection, and increasing yields (by the diversion of assimilates from vegetative to reproductive organs). The nucleic acids may also be used to induce male and/or female sterility (by expression in floral organs), creduce male and/or female sterility (by expression in floral organs), inhibit reversibility in the development or germination of seeds and reduce shoot growth in commercial wood species. Antisense constructs of the nucleic acids can also be used to transform plants to reduce the expression of GA 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set and growth in seedless grapes, citrus fruits and spars), improve skin texture and fruit shape in apples, increase stem length and therefore yield in sugar cane, increase yield and earliness in celery and rhubarb, improve malting yields and quality in cereals (particularly barley), and increase growth in woody species
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Pred. No. 1.2e-103;
0; Mismatches 329;
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produce transgenic plants with improved or altered growth
                                                                                         CCTTTTTCATCAATGTTGGTGACGCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTG
                                                                                                                                                CTICITICITICIAAACGIIGGIGACTCICICCAGGIGAIGACAAAIGGGAGGIICAAAGAGGCG
                                                                                                                                                                                                                                                                                                        rgaggcaragggriniagcraacrgraagaarcragggrincrargarrracrrcgcrg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "Gibberellin 2-oxidase AtGA2ox1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox1 cDNA.
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S Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Kanna, A., Bolla B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Khanna, A., Bolla B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., McCann, R., Waterston, R. Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

I unpublished (1999)
Other ESTS: BYSTOSCT
Unpublished (1999)
Other ESTS: BYSTOSCT
Unpublished (1999)
Other ESTS: Bystosct
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW184969 EST 24-JUL-2004 se84f09.yl Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1410 5' similar to TR:004162 004162 DIOXYGENASE. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone it has been determined, an EST from the other This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 27006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                            CV292117 EST
BIG66577 CMB
BIG646259 EST
BW685035 BW6i
BP074757 BP0
CA844444 EAD
CA844444 EAD
CA844444 EAD
CA84443 EAZ
AW582063 EAZ
AW5820639 EST
CV470333 431.
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BIJ70132 GW83
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AW222239 EST
BQ404995 GA
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/cultivar="T157"
/db_xref="taxon:3847"
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DN982067
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Maximum Match 100%
Listing first 45 summaries
                                                                                         nucleic search, using sw model
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                     GenCore (c) 1993 .
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AUTHORS
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                                     /done liber@mc1023"
//done liber@mc1023"
//done libergweator: pSPORT1; Site_1: Sal1; Site_2: NotI; This colne liberay was constructed from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies

library was prepared using the Life Technologies

SimperScript CDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The CDNA fragments were directionally cloned into the Not I -Sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 ACGCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGACCCCGATGCCAAGACCCA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               384 GGCGATGTCGGTTGGGTCGAATACCTCCTTCTCAACACCAACCCTGATGTCATCTCCCCC 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTACAGCAGTGAAGAACATGTGCTATGCGGTGTTGGAATTGATGGCGGAGGGGTTGGG 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 ATAGTCAATGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCGTTA 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 CAGTICATGGCCAATTIGGAAAACGAAACCTCGGGTICTTCAAAAAACCTCAATCCGAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 GGTGATGTCGGTTGGGTCGAATACCTCCTCAACACCCAACCCTGATGTTATCTCACCC 360
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'tissue_type="seed coats of greenhouse grown plants'
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Pred. No. 1.8e-127;
0; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 87.2%;
Matches 496; Conservative
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BM085298 53-JUL-2004 saj34h07.yl Gm-c1066 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1066-4957 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA

DEFINITION

GI:16995926

sequence. BM085298 BM085298.1 EST.

> ACCESSION VERSION KEYWORDS

```
Contact: Shoemaker K/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD sy006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /GDLELVATE"ULAILLAGUES
//GDLE="SOYBEAN CLONE ID: Gm-c1066-4957"
/clone="SOYBEAN CLONE ID: Gm-c1066-4957"
/tissue type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab host="DH108"
/lab host="DH108"
/lab host="DH108"
/lote="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 0: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 0: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 0: EcoRI; Site 2:
/note="Vector: pBluescript II SK+; Site 0: EcoRI; Site 0: EcoRI; The clow Annual Seedling From the cultivar Williams. The 2 week old seedlings were salt stressed in a solution of 500mM Nacl for 3 days prior to harvesting. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XNoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XNoI diggestion. The cDNA fragments were in the construction of the site of the plant fragments were in the construction of the site of the blunt fragments were in the construction of the site of the blunt fragments were in the construction of the site of the blunt fragments were in the construction of the site of the blunt fragments were in the construction of the site of the blunt fragments were in the construction of the site of the blunt fragments were of the site of the blunt fragments were in the construction of the site of the si
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated CDNA fragments were transformed into DH10B host cells (GibcoBR). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Glycine max (soybean)
Glycine max
Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons,
rosids; eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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Pred. No. 3.1e-124
0; Mismatches 66
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/organism="Glycine max"
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/cultivar="Williams"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.5%;
88.0%;
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Best Local Similarity
Matches 483; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439 ATGTGCTATGCGGTGTTGGATTGATGGCGGAGGGGTTGGGGATAAGGCAGAGAATACG 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATACCTCCTCAACACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC 378
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                    3,
                                                                                                                                                 Length 1365
                                                                                                                                                                                      Indels
                                                                                                                                               Score 424.8; DB 4;
Pred. No. 2.1e-118;
0; Mismatches 297;
                   pnds"
/clone="GSLTFB7ZE01"
/tissue_type="Flowers and /ecotype="Col-0"
/plasmid="pcMVSPORT_6"
                                                                        1. .1365
/gene="At1g30040"
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llarity 67.2%;
Conservative
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. Montation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences): 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length.
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1 (bases 1 to 1365)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Fhll-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
 257
                                                       http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
 GAGTTCATGGCCAATTTGGAAAACGAAACCCTCAGGTTCTTCAAAAAACCTCAGTCCGAC
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/mol_type="mRNA"
/db_xref="taxon:3702"
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HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Crosids: eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (base 1 to 1141)
Castelli, V. Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Crubaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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The sequences are based on single pass reads.

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UKGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences.
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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HTC, GSLT. CDNA.
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BU549366 622 bp mRNA linear EST 16-SEP-2002
GM880016A20B10 Gm-r1088 Glycine max cDNA clone Gm-r1088-5828 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lewin, H. A., Director, Keck Center for Comparative and Functional
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
El: (217) 244-6147
Fax: (217) 333-4582
Email: 1-vodkin@uiuc.edu
                                                                          GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTGGCTGAC
                                                                                                                                                                                                                                                                         822 GCTCTTCAGGTTATGACTAACGGGGGGTTCAAGAGGTGTTAAACACAGGGTCTTAGCCGAT
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                                            CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
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Plate: GM880016A20 row: B column: 10
Seq primer: 5'-TTTTTTTTTTTTTTTT (A/C/G)-3'
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/organism="Glycine max"
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) . 5 prime and 3 prime are assembled with Phrap.
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Location/Qualifiers
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    Combined Approach to Evaluate and Improve Arabidopsis Genome
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set of 9,216 low redundancy clones selected from CDNA libraries from various fissues and steages of development of soybean that consists of 2,706 CDNAs from germinating cotyledons (source libraries Gm-c1027); 1,355 CDNAs from immature seed coats (libraries Gm-c1019 and Gm-c1023); 917 CDNAs from tissue culture derived somatic embryos (source libraries Gm-c1019 and Gm-c1053); 917 CDNAs from tissue culture derived somatic embryos (source libraries Gm-c1067, and Gm-c1067, and Gm-c1067, and Gm-c1067, and Gm-c1068); and 963 CDNAs from young leaves exposed to bacterial and fungal pathogens (source libraries Gm-c1072, dm-c1073, and Gm-c1074). The 5' ESTS of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-c1089 and the CDNA clones of the reracked Gm-r1088 library were then sequencing was funded by NSF Plant Genome project #8872565 (http://soybeangenomics.cropsci.uiuc.edu/) as part of creation of a low redundancy soybean CDNA select shingled by the laboratories of Lila vodkin, University of Illinois, Randy Shoemaker, lowa State University, and Paul Keim, Northern Arizona University, as part of the Public EST project, thtp://lso.186.26.94/soybeanset.html. The contig analysis to select unique genes was performed by the laboratories and Bioinformatics, University of Minnesoca, http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and 3' sequencing were conducted by services of the University of Ernest Retzel, Center for Computational Genomics http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and sequencing were conducted by services of the University of Illinois Keck Center for Computational Genomics http://web.ahc.umn.edu/biodata/nsfsoy/. Reracking and sequencing were conducted by services of the University of Illinois Seck Center for Computational Genomics http://web.ahc.um.edu/biodata/nsfsoy/. Reracking and 3' sequencing were conducted by Services of the University of the original cond information on the source library fo
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                                                       Gaps
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  Score 420.4; DB 5; Length 622;
Pred. No. 3.7e-117;
0; Mismatches 49; Indels 3:
tch 42.2%; al Similarity 89.9%; 461; Conservative
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     Query Match
                              Best Local
Matches 46
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Direct Submission

L. Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

By 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

NRAY INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                              CNSOABKL 1363 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH20ZC07 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Fracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1363)
201 AAAGAATTCACATGGTGGGAATACAAGAAGGCTGCGTAATGCGTCAAGGCTAGCGATAAT 142
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Location/Qualifiers
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/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
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67.0%; Pred. No. 8e-116;
iive 0; Mismatches 296;
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                                                                                        964 AGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
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/db_xref="taxon:3702"
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 ENYE cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librarises construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). Sprime and 3 prime are assembled with Phrap.
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Template, G., Caboche, M., Weiseenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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length
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Location/Qualifiers
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="GSLTFB70ZF11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ecotype="Col-0"
/plasmid="pcMVSPORT_6"
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of strain col-0 of Arabidopsis
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HTC; GSLT_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672
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                                                                                                                      CCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCCAAACGGTGATGTCGGTTGGGGTC
                                                                                                                                                                                                             GAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCCAAATCACTTTGCATTTTC
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                                  GAAAACGAGGCCCTCAGGTTCTTTAAAAATCTCAGTCCGAGAAAGACAGAGCTGGTCCC
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GSLTFB70ZF11 of Flowers and buds
thaliana (thale cress).
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CNSOAC3R
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Length 1339; Indels

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318 432 492 438 552 498 612 558

553 GIGICGIACAAGGIGTIGGAGAIGGITGCCGAAGAACTAGGGATAGAGCCAAGGGACACT

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(bases 1 to 1339)

REFERENCE

499 TTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTGGTGCTTCAGGTTGAACCACTACCCG

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/note="Vector: Bluescript II SK+; Site I: EcoRI; Site_2:
Xho1; The cDNA library was constructed from floral
meristenatic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018 5 05 018, mRNA sequence.
AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone AJ803092.
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 CAGTICATGGCCAATITGGAAAACGAAACCCTCGGGTTCTTCAAAAACCTCAATCCGAG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 AAAGACAGGCCTGGTCCCCCTGACCCTTTTGGCTACGCCAGCAAGAGGATTGGCCCTAAC 450
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 785)
Bey,M., Stueber,K., Fellenberg,K., Schwarz-Sommer,Z., Sommer,H., Saedler,H. and Zachgo,S.
Characterization of Antirrhinum Petal Development and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ATGGTTGTTCTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
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     clone="GENOME SYSTEMS CLONE ID: Gm-c1051-1097"
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                          /tissue_type="floral meristematic mRNA"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%; Score 375.6; DB 2;
88.3%; Pred. No. 2.1e-103;
ive 0; Mismatches 54;
                                                                              /clone_lib="Gm-c1051"
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Antirrhinum majus (snapdragon)
Antirrhinum majus
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Matches 408; Conserv
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           970 GCACCATIGCCATIGCCTIGICCCTGAGCAAGATIGGTGTTIGIGCTTIACAAGAATICACT 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 413.
                                                                                   678
                                                                                                                                                                                                                                                                                                                   849
                                                                                                                                                                                                                                                                                                                                                                                                 910 ACAAGGAGATCGAGGATTTCAATGATATTTCGGCGGACCGCCATTGAGCCAGAAGATC 969
CTGAGTAAAATGCTGAGAGATGAGAAGAGTGACTCGTGCCTGAGACTAAACCATTATCCG 672
                                                                                                                                                                                                       730 ccacadataarcricagigciaagarcraaraacacgggggggcrcricaaarcrigigaaa 789
                                                                                                                                                                                                                                                                GATGGCACTTGGGTTTCAGTCCCACCTGATCAGACTTCCTTTTTCATCAATGTTGGTGAC 738
                                                                                                                                                                                                                                                                                                                                                                 GCTCTACAGGTAATGACTAATGGGAGGTTTAAAAGTGTAAAGCATAGGGTTTTTGGCTGAC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAACGAAGTCAAGGTTATCAATGATCTTTTGCAGGACCAGCGTTGAGTGAAAATATA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACCTTTACCTT -- CAGTGATGTTAAAAGGAGAGAGAGTGTTTGTACAAAGAGTTCACA 915
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                                                                                                                                                      CCACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGCTTGCAAATCTGTCTCACA
                                                                                                                                                                                                                                                                                                             GATGGAAGTTGGGTCGCTGTCCTCGACTCTTTCTTCTTCATTAATGTTGGAGAT
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                CCTTGCCCTGAGGTGCACTGAACCGGAATTTGGTTGGGT
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/mol_type="mRNA"
/cultivar="Corolla"
/db_xref="taxon:3847"
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
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Best Local Similarity 68.4%;
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Genoscope.

Direct Submission

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads

Life Technologies (advision of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Waincker P., Menard M., Cruaud C., URCY INRA : Clept C., Caboche M.

URCY INRA : Clept C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). S prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                           Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                   Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis
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    1128
/organism="Arabidopsis thaliana"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Flowers
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:3702"
/clone="GSLTFB56ZG10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /plasmid="pCMVSPORT (complement(1. .1128)/gene="At1g78440"
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/tissue_type="suspension cultures"
/lab host="SOLR"
/clone_lib="cTOS"
/clone_lib="cTOS"
/clone_lib="cTOS"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with IS$
coconut milk (filter sterilized and added after
autoclaving), 2% saccharose, and lmg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
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    Location/Qualifiers
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                                                                              /organism="Lycopersicon esculentum"
/mol_type="mRNA"
/culfivar="TA496, B6203"
/db xref="taxon:4081"
/clone="cTOS17020"
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Pred. No. 4.8e-91;
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    100 Jordan Hall, Clemson,
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69.6%;
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EST526608 CTOS Lycopersicon esculentum CDNA clone CTOS17020 5' end,
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Lycopersicon esculentum
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Spermatophyta, Magnoliophyta, eudicotyledons; core eudicotyledons;
asterids, lamids, Solanales, Solanaceae, Solanum; Lycopersicon.
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                                                                 ATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCTGATGTTATCTCACCCAAAT 364
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                                                                                                                                                                                                                                                                                  CATCAGTGAGAAAAATGACATTCGATGTTTTGGAGAAGATCACAGATGGGCTAGGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  561 TTAATCACTATCCACCATGTCCTCTTAGCAATAAGAAAACCAATGGTGGTAAGAATGTGA
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Clemson University Genomics Institute
Clemson University
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                                                                                                                                                                                                                                                                                                                                  241 AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC
                                                                                                                                                                                                                                                                                                                                                                 397 AAAGACAGGCTGGTCCCCCTGATCCTTTTGGCTACGCAGGAAGAGGGTTGGCCCTAAC
61 ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGACCACCCCGATGCCAAGAATCTC
                                                                                                               ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG
                                                                                                                                                                                                                        GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GGTGATGTCGGTTGGGTCGAATACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 GGGAIGTCGGGIGGGTCGAATACCTCCTTCTCAACACCAACCCTGACGTCATCTCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 AAATCACTTTGCATTTTCCGAGAAAATCCTCATCATTTCAGGGCGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                         BM893076 5-JUL-2004 sam51f05.y1 Gm-c1069 Glycine max CDNA clone SOYBEAN CLONE ID: Gm-c1069-2961 5' similar to TR:Q9XG83 Q9XG83 GA 2-OXIDASE. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: estewatson wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTS on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stopp: 435.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosida; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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/mol_type="mRNA"

/db xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1069-2961"

/clssue type="legenerating cotyledons, 9-10 day old etiolated seedling"

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/organism="Glycine max"
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                                                                                                                                                                                                                                                  BM893076.1 GI:19348544
                                                                                                                                                                                                                                                                                                     Glycine max (soybean)
Glycine max
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                                                         RESULT 13
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                                                                                  BM893076
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/clone libe "MtBC"
//note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript pSK; Site_1: pBcoisses
//note from sector: pBluescript pSK; Site_1: pBcoisses
//note from Terragreen mix in the presence of onion
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/dev_stage="harvested 3 weeks post inoculation with Glomus
intraradices"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire

Biologie Moleculaire des Relations Plantes-Microorganismes,

CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:

Mt-est@toulouse.inra.fr Website:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gouzy, J., Jaillon, O.,
517 AAGTCACAGTTCATTTTCCGAGAAAGTCCTCAGAATTTCAGGGTGGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula ESTs from endomycorrhizal roots Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 478)
Journet, B.P., Crespeau, H., van-Tuinen, D., Gouzy
Journet, Carreau, V., Chatagnier, O., Kahn, D.,
Gianinazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Medicago truncatula"
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Medicago truncatula
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1 ATGGTTGTTCTGTCTCAGCCAGCATTGGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC

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47;

Score 334.8; DB 3 Pred. No. 6.9e-91; 0; Mismatches 47

33.6%;

Conservative

Matches 363; Query Match Best Local S

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Similarity

DB 3; Length 567; Indels

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/dionellberlate Blight-Challenged Tubers"
//dionellberlate Blusscript II SK(+) KR; Site 1: ECORI;
Site 2: KhoI; supplier: Pathogen-challenge series. Tubers
Site 2: KhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tuberosum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were inocubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 GATCCACAAATTATTTCTTTATTAAGATCCAATAACACTTCTGGACTTCAAATTTACACTT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 GCTTGTGAGATTCTTGAAATGTTAGCAGAGGATTAAAAATTCATCCAAAGAATGTATTT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TACCTCCTCCTCAACACCCAACCCTGATGTTATCTCACCAAATCACTTTGCATTTTCCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AGTAAGCTTTTAATGGATGAAAAAGTGATTCACTTTTTAGGCTAAATCATTACCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCCCTGAGG-----TGCAAGCACTGAACCGGAATTTGGTTGGGTTTGGGGAGCACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 TGTCCTGATGAATTTCAAGAATATAATGGAAGAAATTTAATTGGATTTGGTGAACATACT
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                                                             organism="Solanum tuberosum"
                                                                                                                                                                                                                 /tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                       db_xref="taxon:4113"
Location/Qualifiers
                                                                                          /mol_type="mRNA"
/cultivar="Shepody"
                                                                                                                                                                                       /clone="50141"
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50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
50141.5', mRNA sequence.
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1 (bases 1 to 893)
Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S. Gneration of ESTs from late blight-challenged potato tubers
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                         RNA was extracted from whole root systems. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into Uni-zap RR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exhssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of
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   phosphate but with a high level of nitrate. After 3
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The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bioatlantech.nb.ca
                                                                                                                                                                                                                                                                                                                                                                                                     Score 332.8; DB 1; Length Pred. No. 2.7e-90; 0; Mismatches 72; Indels
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Matches 395; Conservative
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./cgn2_6/ptcdata/1/ina/5_COMB.seq:*
./cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
./cgn2_6/ptcdata/1/ina/RB_COMB.seq:*
./cgn2_6/ptcdata/1/ina/H_COMB.seq:*
./cgn2_6/ptcdata/1/ina/PCTUS.COMB.seq:*
./cgn2_6/ptcdata/1/ina/PE_COMB.seq:*
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./cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
./cgn2_6/ptcdata/1/ina/RE_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-614-912-13
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US-09-719-108-9
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Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
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Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 12, Appli Sequence 13, Appli Sequence 11, Appli Sequence 14, Appli Sequence 14, Appli			Length 1318; Indels 0; Gaps 0;	CAAGTCC 6	CCCCGATGCCAAGAATCTC 12	GAACCATGGTGTTCCATTG 	GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCGGG 240 	30
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Sequence Sequence Sequence

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TYPE: DNA
ORGANISM: Glycine max
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Patent No. 6723897
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kemmeth J.
APPLICANT: Filler, Kemmeth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Blich, Tedd D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Sherry J.
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
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                                      Gaps
                                  3;
 Length 1359;
                                  Indels
Score 827.4; DB 3;
Pred. No. 3.5e-268;
1; Mismatches 97;
 Query Match
Best Local Similarity 89.9%;
Matches 898; Conservative
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736 CCACAGATAATCTCAGTGCTAAGATCTAATAACACGGGGGGTCTTCAAATCTGTGTGAAA 795
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Pred. No. 3.8e-131;
0; Mismatches 326;
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APPLICANT: Lee, Jian Ming
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APPLICANT: Meng, Zude
APPLICANT: Name Belain Betabolism Genes
FILE REFERENCE: BB1379 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR PILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-21
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
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Best Local Similarity 65.7
Matches 652; Conservative
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; ORGANISM: Glycine max
US-09-614-912-13
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                               1062 GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCTGAT 1100
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Pred. No. 3.5e-132;
0; Mismatches 291;
  GATAATAGGCTTGCCCCTTTCCAGAAATCTGCTGCTGAT
                                                                                                                                                                                                                APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 6623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 1999-6-11
PRIOR FILING DATE: 1999-6-11
PRIOR FILING DATE: 1999-6-12
PRIOR APPLICATION NUMBER: GB 98126218
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 16
SOFFWARE: PatentIn Ver. 2.1
                                                                                                                                                                        Sequence 7, Application US/09719108
Patent No. 6670527
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; ORGANISM: Arabidopsis thaliana
US-09-719-108-7
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Best Local Similarity 67.5%;
Matches 612; Conservative
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CURRENT APPLICATION NUMBER: UNA
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
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PRIOR FILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-30
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-12-15
PRIOR PLING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PLING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR PLING DATE: 1999-12-21
                                               APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1778 US NA
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Best Local Similarity 65.6%;
Matches 651; Conservative (
                 Famodu, Omolayo O.
                               Lee, Jian Ming
Sakai, Hajime
Weng, Zude
 Miao, Gou-Hau
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                                                                                                                                GAGTTAATGGCCAATTTAGAAAACGAGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 240
ACCCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC 120
                                                                  ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 180
                                                                                       339 gaagcrararccaarragaarargaagccrrcaarrcrrcrrargracrcaargaa 398
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                          219 ACCAAATTTTCCTCAACAATTCCCATAGTGGACCTCTCCAAACCTGATGCAAAGACCTT
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                                                      Indels
Score 419.8; DB 3;
Pred. No. 1.3e-130;
0; Mismatches 327;
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Sequence 5, Application US/09614912 Patent No. 6677502 GENERAL INFORMATION: APPLICANT: Rafalski, Antoni

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APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT PEPLICATION NUMBER: US/09/719,108
CURRENT PELLING DATE: 2000-12-08
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
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US-09-719-108-9
; Sequence 9, Application US/09719108
; Patent No. 6670527
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                                                                                           TTTGGGGAGCACACACACACACACAGATAATTTCTGTCTTAAGATCTAACAGCACATCTGGC
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Sherry J.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBF.216
CURRENT APPLICANTON WHERE: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENTH: 1403
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Pred. No. 4.7e-130;
0; Mismatches 318; Indels 18;
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Matches 657
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Ee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Galmi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB139 US NA
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: B1399 US NA
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR PELING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-11
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
NUMBER OF SEQ ID NOS: 204
                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09614912
Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
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Best Local Similarity
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                                                                                         979 CAGAAA 984
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PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Arabidopsis thaliana
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Best Local Similarity 64.73
Matches 586; Conservative
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APPLICANT: Hedden, Peter
TAPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0633.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: GENSTREAM PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-12
PRIOR FILING DATE: 1998-06-12
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PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
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US-09-719-108-5
; Sequence 5, Application US/09719108
; Patent No. 6670527
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Query Match 35.8%; Score 356.6; DB 3; Best Local Similarity 63.2%; Pred. No. 2.8e-109; Matches 586; Conservative 0; Mismatches 329;
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APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
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Patent No. 6677502
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Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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Rafalski, Antoni
Orozco, Buddy
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CURRENT PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-12
PRIOR PELING DATE: 1999-07-30
PRIOR FILING DATE: 1999-17-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
                                                                                                                                                                                                                                                             APPLICANT: Lee, Jian Ming
APPLICANT: Sakai, Halime
APPLICANT: Weng, Zude
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TILLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
Sequence 3, Application US/09614912
Patent No. 6677502
                                                                                               Allen, Steve
Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
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Best Local Similarity 60.9
Matches 598; Conservative
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ORGANISM: Oryza sativa
                                                                 GENERAL INFORMATION:
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AATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGGGGGTGTTTGTACAAAGAGTTC 912
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Hick, Gregory R.
APPLICANT: Kishore, Gamesh M.
APPLICANT: Elich, Tedd D.
APPLICANT: Loguech, Eugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: RepublicANT: New Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: RepublicANT: New Joel E.
APPLICANT: RepublicANT: New Joel E.
APPLICANT: PLILIG DATE: 1999-08-10
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILLING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 5.8e-93;
0; Mismatches 167; Indels
                                                                                                                                                                                                                          Sequence 67, Application US/09371307A Patent No. 6723897
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ORGANISM: Gossypium hirsutum
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Matches 436; Conservative
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COTHER INFORMATION: n
US-09-371-307-67
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US-09-371-307-67
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                                                                                                                                                 31.5%; Score 314.2; DB 3; Length 1555; 59.3%; Pred. No. 6.3e-95; ive 0; Mismatches 383; Indels 12;
                                                                                                                                             Query Match
Best Local Similarity 59.3
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   ; TYPE: DNA; CORGANISM: Zea mays US-09-614-912-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ACCAATCAAGAACACAACT------TCTCTGTTTATGGCAAAAACCCTGAGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 gagrirganggcagaagggrirgaagarrcagcaaaaggargrirnagcaagcrrcraarg 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 GGTAGCAAGAGGATTGGCCCAAACGGTGATGTCGGTTGGGTCGAATACCTCCTCAAC 336
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filer, Kenneth J.
APPLICANT: Kichore, Ganesh M.
APPLICANT: Kichore, Ganesh M.
APPLICANT: Bao, Sudabathula
APPLICANT: Logusch, Bugene W.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFRENCE: MOSP: 129
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                    958 GATAATAGGCTTGCCCCTTTCCAGAA
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Best Local Similarity 63.2
Matches 261; Conservative
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COTHER INFORMATION: n = a,
US-09-371-307-66
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ORGANISM: Glycine
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US-09-371-307-68
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                                    ACATGGTGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCC 972
                                                                                592 ACTIGGIICGAGIACAAGAAAICIGCIIAIAAFIICCAGAIIGGCAGAIAAAIAGGCICAII 651
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; Sequence 71, Application US/09371307A
; Patent No. 6723897
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Piller, Kenneth J.
APPLICANT: Filor, Tedd D.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Ream, Joel E.
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBF: 1999-08-10
; CURRENT APPLICATION NUMBER: US/09/371,307A
; UNMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
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Matches 316, Conservative
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ORGANISM: Zea mays
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                                                     APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filter, Kenneth J.
APPLICANT: Richore, Ganesh M.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Roo, Sudabathula
APPLICANT: Roo, Sudabathula
APPLICANT: Roo, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
TITLE OF INVENTION: Methods for controlling gibberellin levels
TITLE OF STERENCE: MOST: 1999-08-10
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 68
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Sequence 68, Application US/09371307A Patent No. 6723897 GENERAL INFORMATION:
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NAME/KEY: unsure
LOCATION: (306)
OTHER INFORMATION: n = a, c,
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Best Local Similarity 66.6
Matches 279; Conservative
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Sequence 62, Appl
Sequence 1350, Ap
Sequence 7, Appl
Sequence 64, Appl
Sequence 21951, Ap
Sequence 21951, A
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 7, Sequence 7, Sequence 7, Sequence 18659, Appl
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Sequence 67, Appl
Sequence 141, Appl
Sequence 141, App
Sequence 1278, Ap
Sequence 7861, Ap
Sequence 7861, Ap
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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Query Match Query Match Best Local Similarity 100.0%; Pred. No. 18 1, Length 999; Best Local Similarity 100.0%; Pred. No. 18 1 and Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 and CTTCTCTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC 60 1 And CTTCTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC 60 Qy 61 ACGCCTTGTTCACGGGGAATTCCTGTGAACCAGCCCCGATGCCCAAGAATCTC 120	A 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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	THE PRODUCTION
Application US/10821711 No. US20040237142A1 No. US20040237142A1 Gilbertson, Larry A Krieger, Elysia K Ye, Woong Zhang, Wanggen NVENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS ENCE: 38-21(52967)B PLICATION NUMBER: 05/10/821,711 LING DATE: 2003-04-09 NG DATE: 2003-04-09 SEQ ID NOS: 16 Phaseolus coccineus	
pplication US/10821711 o. US20040237142A1 MATION: Larry A Krieger, Elysia K Ye, Xudong ENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION ENTION: COMMERCIALLY VIABLE TRANSGENIC PLANTS ESTION NUMBER: US/10/821,711 NG DATE: 2004-04-08 ATION NUMBER: 60/461,459 DATE: 2003-04-09 Q ID NOS: 16 haseolus coccineus	67680 20123 42166 10886
14.1 2478 7 US-10-437-963-20123 Sequence 20123, 12.9 457 7 US-10-424-599-42166 Sequence 20123, 12.8 597 7 US-10-424-599-108868 Sequence 108868, Sequence 108868	58, 453, 6766
15.1 966 6 US-10-401-312-58 15.1 966 6 US-10-321-58 14.7 322 7 US-10-40-453 Sequence 453, Apr 14.1 2478 7 US-10-424-599-67680 12.9 457 7 US-10-424-599-42166 12.8 597 7 US-10-424-599-108868 Sequence 20123, 12.8 597 7 US-10-424-599-108868  PPLICATION: ALIGNMENTS ALIGNMENTS  ALIGNMENTS  ALIGNMENTS  ENTION: COMERCIALLY VIABLE TRANSGENIC PLANTS  CE: 38-21(5297)B  ATION UNDER: US/10/821,711  NG DATE: 2004-04-08  ATION UNDER: 60/461,459  DATE: 2003-04-09  Q ID NOS: 16  haseolus coccineus	, 88 58,
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                                                     atch 100.0%; Score 996; D cal Similarity 100.0%; Pred. No. 0; 996; Conservative 0; Mismatches
  ; LENGTH: 1318
TYPE: DNA
; ORGANIEM: Phaseolus coccineus
US-10-670-454-1
LENGTH: 1318
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Best Local S:
Matches 996
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| Publication No. US20040229357A1
| GENERAL INFORMATION:
| APPLICANT: Thomas, Stephen G
| APPLICANT: Thomas, Stephen G
| APPLICANT: Hedden, Peter APPLICANT: Phillips, Andrew L
| TILLE OF INVENTION: Gibberellin 2-Oxidase FILE REFERENCE: 0623.0970000
| CURRENT APPLICATION NUMBER: US/10/670,454 |
| CURRENT APPLICATION NUMBER: US/09/719,108 |
| PRIOR APPLICATION NUMBER: PCT/GB99/01857 |
| PRIOR FILING DATE: 2000-12-08 |
| PRIOR FILING DATE: 1999-06-11 |
| PRIOR PILING DATE: 1999-06-11 |
| PRIOR PILING DATE: 1998-06-12 |
| PRIOR FILING DATE: 1998-07-15 |
| NUMBER: OSEQ ID NOS: 16 |
| SEQ ID NO 1
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162 ACGCCCTTGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCCGATGCCAAGACCCAC 221
                                                                                762 GGCCTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCTGTCCCACCTGATCAAACTTCC
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; Sequence 62, Application US/10401321
; Publication No. US20030233679A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Filer, Kenneth J.
; APPLICANT: Elich, Tedd D.
; APPLICANT: Rao, Sudabathula M.
; APPLICANT: Logusch, Bugene W.
; APPLICANT: Logusch, Sherry J.
; APPLICANT: Bacrson, Scott R.
; TITE OF INVENTION: Methods for Controlling Gibberellin Levels
; FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
; CURRENT APPLICATION NUMBER: US/10/401,321
; UNMBER OF SEQ ID NOS: 89
; SOFTWARE: Patentin version 3.2
; LENGTH: 1359
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89.9%; Pred. No. 1.7e-270;
ive 1; Mismatches 97;
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Piller, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
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Pred. No. 1.7e-270;
1; Mismatches 97;
                                                                                                                                                                                  Sequence 62, Application US/09371307A Patent No. US20020053095A1 GENERAL INFORMATION:
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89.9%;
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CORGANISM: Glycine max
US-09-371-307-62
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Best Local Similarity
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                                                                                                                                                                                                                                                                                              79 ATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTCATAGTGAACGCCTGTAGG
                                                                                                                                                                                                                                                                                                                      211 gagcaggaggcrarregcrrcrrcgccrrgccrcagrcrcrraaaaaccggccggrcca
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                                                                                                                                                                                                                                                                                                                                                                                                     151 dagricegerrerrenaegregranaeceaegagreceaecegaacreargaeregerra
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                                                                                                                                                                                                                      Length 1026;
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                                                                                                                                                                                                                      Query Match 42.6%; Score 424.4; DB 3; Best Local Similarity 67.5%; Pred. No. 4.7e-133; Matches 612; Conservative 0; Mismatches 291;
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; LENGTH: 1026
                                                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                    US-09-938-842A-1350
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Batent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866
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                                                                                              <u> AAAGACAGAGCTGGTCCCCCGGCCCTTTCGGCTATGGTAGCAAGAGGTTGGCCCAAAC</u>
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                                                                                                 ACAACGAAGTCAAGGTTATCAATGATCTACTTTGGAGGACCAGCGTTGAGTGAAATATA
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42.6%; Score 424.4; DB 8; Length
Best Local Similarity 67.5%; Pred. No. 5.3e-133;
Matches 612; Conservative 0; Mismatches 291; Indels
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Publication No US20040229357A1
GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVERTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT APPLICATION NUMBER: US/09/719,108
FRIOR FILING DATE: 2003-09-26
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR PRILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 7
SEQ ID NO 7
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211 GAGCAGGAGGCTATTGGCTTCTTGGCTTGAGTCTCTTAAAAACGGGGCGGTCCA 270
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US-09-938-842A-1350
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                                                                                                                                                                                        Length 1403;
                                                                                                                                                                                        Score 418.2; DB 3;
Pred. No. 7.4e-131;
0; Mismatches 318;
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66.2%;
                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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657; Conservative
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  NUMBER OF SEQ ID NOS:
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; ORGANISM: Glycine US-09-371-307-64
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US-09-371-307-64
i Sequence 64, Application US/09371307A
j Patent No. US20020053095A1
j GENERAL INFORMATION:
APPLICANT Brown, Sherri M.
APPLICANT Heck, Gregory R.
APPLICANT Hiler, Kenneth J.
APPLICANT Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Brown, Joel E.
APPLICANT: Rao, Sudabathula
APPLICANT: Roguech, Sherry J.
APPLICANT: Roguech, Sherry J.
APPLICANT: Roguech, Sherry J.
APPLICANT: Roguech, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBF:216
GURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBURE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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US-10-424-599-21951
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APPLICANT: Elich, Tedd D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Rea, Sudabathula
APPLICANT: Rea, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Barson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 12999.0216.DVUS01 (MOBT:216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
                                                                                                                                                                                                       AATAGGCTTGGACATTTTGAGAGAATTGTTGCT 1123
                                                                                                                               AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT 993
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/10401321
Publication No. US20030233679A1
GENERAL INFORMATION:
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APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Kilshore, Ganesh M.
APPLICANT: Elich, Tedd D.
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 64
LENGTH: 1403
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; ORGANISM: Glycine max
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              PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-670-454-9
FILING DATE: 1999-06-11
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                    GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG
                                                GAGAAAAAAGTAGGACCTCCCAATCCATTGTTGGGTGTAGCAAGAAAATTGGACACAAT
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APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REPERROCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/10/670,454
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR PILING DATE: 2000-12-08
PRIOR PLLING DATE: 2000-12-08
PRIOR PAPLICATION NUMBER: US/09/719,108
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APPLICANT: Tanaka, Hiroshi
APPLICANT: Tanaka, Hiroshi
APPLICANT: Aryano, Toshiaki
APPLICANT: Matsuoka, Makoto
APPLICANT: Matsuoka, Makoto
APPLICANT: Sakamoto, Tomoaki
APPLICANT: Sakamoto, Tomoaki
APPLICANT: Sakamoto, Tomoaki
APPLICANT: Sakai, Miho
TILLE OF INVENTION: GIBBERELLIN 2-OXIDASE GENE, FUNCTIONS AND USES THEREOF
FILE REFERENCE: SHZ-014
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT APPLICATION NUMBER: US/202-276051
FRIOR PILING DATE: 2002-09-20
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH. 984
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   485 GGCAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGT
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60.9%; Pred. No. 4.8e-109;
cive 0; Mismatches 375; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.9°
Matches 598; Conservative
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ORGANISM: Oryza sativa
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OTHER INFORMATION:
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   TGTGAATACAAGAAGGCTGCGTACACTTCAAGGCTAGCTGATAATAGGCTTGCCCCTTTC
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                                                             913 TCTCAATACAAGTTATCTGCTTACAAAACTAAGGCTTGGTGACTATAGGCTTGGTCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Helden, Peter
APPLICANT: Helden, Peter
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver: 2.1
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NAME/KEY: misc feature
LOCATION: (1243, 1265)
OTHER INFORMATION: unidentified residue
US-10-670-454-5
                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/10670454
Publication No. US20040229357A1
GENERAL INFORMATION:
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LENGTH: 1318
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; Sequence 78659, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J.

RESULT 14 US-10-437-963-78659

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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Bucharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1010/437,963
CURRENT APPLICATION UNDER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 78659
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Publication No. US20040214272A1
GENERAL INFORMATION.
APPLICANT: AND GENERAL INFORMATION.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION.
FILE REPERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NOS: 369326
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Sequence 15, Appl
Sequence 19, Appl
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Sequence 140, Appl
Sequence 122, Appl
Sequence 132, Appl
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US-11-152-892-3
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US-11-117-187-209
US-11-117-908-140
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US-11-117-187-212
US-10-750-185-56890
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US-10-995-561-1325
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4.0%; Score 40; DB 7; Length 1011;
Best Local Similarity 53.1%; Pred. No. 0.0025;
Matches 85; Conservative 0; Mismatches 75; Indels
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                                                                                                      Sequence 3, Application US/11152892

Sequence 3, Application US/11152892

Bublication No. US20050251883A1

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Amasino, Richard M.

APPLICANT: Michaels, Scott D.

APPLICANT: Michaels, Scott D.

TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants

FILE REFERENCE: 960296.97665

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT FILING DATE: 2005-06-15

PRIOR FILING DATE: 2002-05-23

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 3

LENGTH: 1011

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Publication No. US20050251883A1
GENERAL INFORMATION:
APPLICANT: Anasino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Bizzall, Scott D.
APPLICANT: Bizzall, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REPERENCE: 960296, 37605
CURRENT FILING DATE: 2005-06-15
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/10/155,435
SPRIOR PILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
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US-11-152-892-2
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; LOCATION: (1)..(1008)
US-11-152-892-3
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LENGTH: 3861
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112 AAGAATCTCATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGT 171

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2392 ACAAAAATAAAGCAAAGAGTGTTAGTTGATACAAAATAATGAGATTTTACAGTATGGAT 2333
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                                                            254 ATATCAATGGATGTTGGAGAAGATGAGACAAGAGCAAATTAGGGTCTTTAGAGAGCCT 313
172 GITCCATTGGAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCT
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Pred. No. 0.21;
0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REPERENCE: 04-164-US
CURRENT APPLICATION WUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR PILING DATE: 2004-04-22
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-13
PRIOR PILING DATE: 2004-04-11-30
PRIOR RILING DATE: 2004-01-10
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,826
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/633,826
PRIOR FILING DATE: 2004-11-30
SOFTWARE: PatentIn version 3.3
SEQ ID NO 44
TURNER DATE: LISA 37
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APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
CURRENT PILING DATE: 2005-04-22
PRIOR APPLICATION NUMBER: US 60/564,758
PRIOR PILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR PILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR FILING DATE: 2004-10-07
PRIOR FILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
PRIOR PILING DATE: 2004-11-30
PRIOR FILING DATE: 2004-11-30
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Publication No. US20050260659A1
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Best Local Similarity 58.8%;
Matches 67; Conservative (
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CORGANISM: Homo sapiens
US-11-112-908-44
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US-11-117-187-209
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                                                                                                         Query Match 3.9%; Score 38.8; DB 7; Length 182314; Best Local Similarity 58.8%; Pred. No. 0.24; Matches 67; Conservative 0; Mismatches 47; Indel8 0;
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APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: 08/11/152,892
CURRENT FLING DATE: 2005-06-15
PRIOR FILING DATE: 2005-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/11174166
Publication No. US20050260669A1
GENERAL INFORMATION:
APPLICANT: Kirsch, Wolff M.
APPLICANT: Lennart, Anton
APPLICANT: Kelln, Wayne J.
APPLICANT: Kelln, Rayne J.
APPLICANT: Levine, Reackyung
APPLICANT: Levine, Rodney L.
APPLICANT: Rouault, Tracey
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Publication No. US20050251883A1
GENERAL INFORMATION:
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SEQ ID NO 1
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                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-45
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; ORGANISM: Arabidopsis
US-11-152-892-1
LENGTH: 182314
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PPLICANT: COPENSHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851 AAAATATAGCACCTTTACCTTCAGTGATGTTAAAAGGAGGAGGAGTGTTTGTACAAAGAGT
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TITLE OF INVENTION: IRON REGULATING PROTEIN-2 (IRP-2) AS TITLE OF INVENTION: A DIAGNOSTIC FOR NEURODEGENERATIVE DISEASE FILE REFERENCE: LOMAU.140C uS/11/174,166 CURRENT APPLICATION NUMBER: uS/11/174,166 PRIOR PAPLICATION NUMBER: 60/222,863 PRIOR PAPLICATION NUMBER: 60/222,863 PRIOR PAPLICATION NUMBER: 00/222,863 PRIOR FILING DATE: 2000-08-04 NUMBER OF SEQ ID NOS: 20 SOFTWARE REALSEQ for Windows Version 4.0 SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1751 GIGTGTAGGAAATACAGCACCTTTATCAGAAGCAATTTTGAATGCAG 1797
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Pred. No. 0.35;
0; Mismatches
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Publication No. US2050260659A1
GREAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TILE OF INVENTION: Breast Cancer Biomarkers
FILE REFERENCE: 04-164-US
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CURRENT FILING DATE: 2005-04-28

PRIOR APPLICATION NUMBER: US/09/531,120

PRIOR FILING DATE: 2000-03-17

PRIOR PLILING DATE: 1999-03-18

NUMBER OF SEQ ID NOS: 212

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 209

LENGTH: 611587
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US-11-117-187-209
                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%;
                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Rattus Norvegicus
US-11-174-166-19
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Matches 62; Conservative
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                                    501 AAGCAGGTTGCTGAAGGATGAGAAAAGTGATTC
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Best Local S
Matches 58
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Pred. No. 26;
0; Mismatches 75; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.3%; Score 33; DB 7; Length 921; Best Local Similarity 51.0%; Pred. No. 0.66; Matches 78; Conservative 0; Mismatches 75; Indels
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Publication No. US2005026055941
GENERAL INFORMATION:
APPLICANT: Harris, Cole
APPLICANT: Davis, Lisa M.
TITLE OF INVENTION: Breast Cancer Biomarkers
FILE REFERRENCE: 04-164-US
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT APPLICATION NUMBER: US 60/564,758
PRIOR APPLICATION NUMBER: US 60/575,978
PRIOR FILING DATE: 2004-04-23
PRIOR FILING DATE: 2004-06-01
PRIOR FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR APPLICATION NUMBER: US 60/631,702
PRIOR SELING DATE: 2004-11-30
PRIOR SELING DATE: 2004-11-30
PRIOR SEQ IN NUMBER: US 60/633,826
PRIOR SEQ IN NOS: SII 1
SOFTWARE: PATENT VARIATION 3
CURRENT APPLICATION NUMBER: US/11/112,908
CURRENT FILING DATE: 2005-04-22
PRIOR PLICATION NUMBER: US 60/564,758
PRIOR FILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-06-01
PRIOR PILING DATE: 2004-11-30
SOFTWARE: PATENT NUMBER: US 60/633,826
NUMBER OF SEQ ID NOS: 511
SOFTWARE: PATENT NOS: 511
SOFTWARE: PATENT NETALING 3: 2004-12-07
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Best Local Similarity 51.۰۰
Best Ag, Conservative
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CRGANISM: Homo sapiens
US-11-112-908-40
                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-140
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104835 TAAAAAAGGAAAAGACTAGTTTTTTTTATTACAACAACCTCACAAACACCAATGATCT 104894
                                     | FULLICARION NO. USZUCUSUZEBSENAI |
| GENERAL INFORMATION |
| APPLICANT: COPENIAVER, GREGORY |
| TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS |
| FILE REFERENCE: ARCD: 30905 |
| CURRENT APPLICATION NUMBER: US/11/117,187 |
| CURRENT APPLICATION NUMBER: US/09/531,120 |
| PRIOR FILING DATE: 2000-03-17 |
| PRIOR FILING DATE: 1999-03-18 |
| NUMBER OF SEQ ID NOS: 212 |
| SEQ ID NO 212 |
| SEQ ID NO 212 |
| LENGTH: 163317 |
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APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: DENISE, Sue K.
APPLICANT: RERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMIL100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
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57.4%; Pred. No. ...
... 0; Mismatches
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PRIOR FILING DATE: 2002-12-31
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; Sequence 212, Application US/11117187; Publication No. US20050266560A1
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US-10-750-185-56890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Arabidopsis thaliana US-11-117-187-212
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 56890
LENGTH: 1138
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                                                                                                                                                                                         223 AAGAACATTCCACGTGAAAAGAATATGAACACCAAGGGCTTGAGTTGAGAGGGGCCAGTG 164
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PREUSS, DAPHNE
APPLICANT: PREUSS, DAPHNE
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
FILE REFERENCE: ARCD:309US
CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR APPLICATION NUMBER: G0/125,219
PRIOR PILING DATE: 1999-03-18
                                                               CAGAGGAATACGTTAAGCAGGTTGCTGAAGGATGAGAAAAGTGATTCGTGCTTCAGGTTG
                                                                                                                                                  142 TTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTGGAGTTAATGGCCAATTTAGAA
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Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
TITLE REFERENCE: 091386.6000-00000.
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
FRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN VETSION 3.3
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3.2%; Score 31.6; DB
Best Local Similarity 55.5%; Pred. No. 53;
Matches 61; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 199, Application US/11117187
Publication No. US20050266560A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Arabidopsis thaliana US-11-117-187-199
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                                                                                                                                                                                                                                     GAGCACACAG 616
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SOFTWARE: Patentin Ver. 2
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; ORGANISM: Homo sapiens
US-11-121-086-44
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LENGTH: 101786
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NAME/KEY: misc feature

LOCATION: (1)....(187786)

COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-: US-10-995-561-13474
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TILE REPERENCE: CLOOJUSS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER: OF SEQ ID NOS: 85702
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 13474
LENGTH: 187786
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   DB 7; Length 167116;
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54.9%; Pred. No. 94;
tive 0; Mismatches 51; Indels 0;
                                                             56; Indels
3.2%; Score 31.4; Digerry Match
Best Local Similarity 53.7%; Pred. No. 87;
Matches 65; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13474, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
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Best Local Similarity 54.9
Matches 62; Conservative
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ORGANISM: Homo sapiens
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US-10-995-561-13474/c
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Title: Perfect score:

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AX302041 Cucurbita AK506655 Sequence BT004464 Arabidops BD243013 Enzyme. 7 AR444995 Sequence AX008677 Sequence AX008677 Sequence AR52813 Vigna ang AR52813 Sequence AR52817 Sequence AR52818 Sequence AR060391 Lotus sat AK101382 Pisum sat AK660714 Oryza sat AK060714 Oryza sat AK06066 Oryza sat AK101713 Oryza sat AK101713 Oryza sat AK101713 Oryza sat AK099350 Oryza sat AK099350 Oryza sat AR099350 Oryza sat AR099350 Oryza sat AR099350 Oryza sat AR0931207 Latusa sat AR52815 Sequence
AX008671 Sequence
A132438 Phaseolus
AB181372 Vigna ang
AR528429 Sequence
AX59429 Nerium ol
AB125232 Nicotiana
AV588978 Nerium ol
Y09113 Minacrocarp
AJ315663 Cucurbita
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phaseolus coccineus bubantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Phaseolus.
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Dna constructs and methods to enhance the production of commercially viable transgenic plants
Patent: WO 2004092390-A 3 28-OCT-2004;
Monsanto Technology LLC (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:3886"
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Sequence 3 from Patent WO2004092390.
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5 AB181373
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AR452811
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ATH132436
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AB125232
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Location/Qualifiers
        Phaseolus coccineus
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VERSION
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AUTHORS
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-Q=/cgn2_1/USPTO spool/US10670454/runat_27122005_124840_29099/app_query.fasta_1.519
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-FGAPPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BD243009 Enzyme. 7
AR444991 Sequence
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(c) 1993 - 2005 Compugen Ltd.
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Datent: JP 2002518005-A 1 25-JUN-2002;
THE UNIVERSITY OF BRISTOL

OS Phaseclus coccineus (scarlet runner bean)
PN JP 2002518005-A/1
PD 25-JUN-1099 JP 200554838
PR 12-JUN-1999 GB 9812821.8,15-JUL-1998 GB 9815404.0 PI
STEPHEN GREGORY THOWAS, PETER HEDDEN, ANDREW LEGNARD PHILLIPS PC
C12N15/09, A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10, PC
C12N15/09, PC C12N15/00,C12N15/00
CC Enzyme
FR Key
I. 1318
FT source /organism='Phaseolus coccineus (scarlet runner)
                                                                                                                                                                                                                                                                                                                                                                                                    coccineus (scarlet runner
                                                                                                    BD243009.1 GI:33052779
JP 2002518005-A/1.
Phaseolus coccineus
Phaseolus coccineus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Pabales; Fabaceae; Papilionoideae; Phaseoleae;
Phaseolus.
I (bases 1 to 1318)
Thomas, S.G., Hedden, P. and Phillips, A.L.
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//organism="Phaseolus coccineus"
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/db_xref="taxon:3886"
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             961 AATAGGCTTGCCCCTTTCCAGAAATCTGCTGCT
  321 AsnArgLeuAlaProPheGlnLysSerAlaAla
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Thomas, S.G., Hedden, P. and Phillips, A.L. Gibberellin 2-oxidase
Patent: US 6670527-A 1 30-DEC-2003;
The University of Bristol; Bristol;
GBX;
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Sequence 1 from patent US 6670527.
AR444991. GI:42672879
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PC0132438 1318 bp mRNA linear PLN 20-APR-1999 Phaseolus coccineus mRNA for GA 2-oxidase, gene ga2ox1.
AJ132438.1 GI:4678585
AJ132438.1 GI:4678585
Phaseolus coccineus
Phaseolus coccineus
Phaseolus coccineus
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermarophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
Ashton Research Station, Long Ashton Research Station, Bristol,
                                                                                                                                                                                                                                                                         261 HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro
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/ db_xref="taxon:3886" |
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10200325
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Phillips, A.L.
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PHILLIPS ANDREW LEONARD (GB); HEDDEN PETER (GB); UNIV BRISTOL (GB);
THOMAS STEPHEN GREGORY (GB)
LOCALION/Qualifiers
                                                                              PAT 06-SEP-2000
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosids I, Pabales, Pabaceae, Papilionoideae, Phaseoleae,
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 AATAGGCTTGCCCTTTCCAGAAATCTGCTGCT 1060
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Enzyme
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Sequence 1 from Patent W09966029,
AX008671 GI:9996195
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/product="gibbre11in 2-oxidase"
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/protein id="BAD99507.1"
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/brotein id="BAD99507.1"
/brotein id="BAD99507.1"
/crein id="BAD9507.1"
/crein i
                                                                                                                                                                                                                                                                                                                                                                                                            AB181372 1360 bp mRNA linear PLN 09-JUN-2005 Vigna angularis VaGA20xAl mRNA for gibberellin 2-oxidase, complete cds.
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Nakajima, M., Xu,Z., Park,S., Tomioka,K., Sakane,M. and Yamaguchi,I.
Direct Submission
Direct Submission
Submitted (08-J7M-2004) Masatoshi Nakajima, The University of
Tokyo, Dept. Appl. Biol. Chem., Fac. of Agriculture; 1-1-1 Yayoi,
Bunkyo, Tokyo, 113-8657, Japan
(B-mail:hhym@pgrl.ch.a.u-tokyo.ac.jp, Tel:81-3-5841-5192,
Pax:81-3-5841-6025)
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Unpublished
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Vigna angularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.
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                                                   TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAgp
                      HisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro
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1. 1360
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/db_xref="taxon:3914"
/clone="vagA2oxA1"
/dev_stage="etiolated eg
/country="Japan"
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Pred. No.:
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                                           CATAGGGTTTTGGCTGACCAACGAAGGACTATCAATGATATACTTTGGAGCCA
                                                                        203 ATACTGGAGGCCTGTAGGGACTACGGCTTCTTCAAGCTCGTGAACCATGGTGTTCCATTG
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Mismatches:
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                                                                                                      Logusch, E.V
Baerson, S.I
 PAT
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Brown,S.M., Elich,T.D., Heck,G.R., Kishore,G.M.,
Logusch,S.U., Piller,K.J., Rao,S., Ream,J.E. and
Methods for controlling gibberellin levels
Patent: US 6723897-A 62 20-APR-2004;
Monsanto Technology, LLC; St. Louis, MO
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
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Sequence 62 from patent US 67.
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AR528429.1 GI:53916494
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Length:
Matches:
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Mismatches:
Indels:
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TSGLQIQLKOGSWIISTPPDQSSFFINYGDSTQVITNGSFKSYKHKANTANSMKSRLSNI
YFGGPPLSEKIAPLFSLAMEGEDSIXKEFTWFEYKKSAYKSRLADNRLVLFEKIAAS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-APR-2004) Instituto de Biologia Molecular y Celular de Plantaes, Consejo Superior de Investigaciones Científicas (CSIC). Universidad Politecnica de Valencia, Avda. de los Naranjos s/n, Valencia 46022, Spain
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                                                                                                                                                                                                                                                                                              1002 TTCTACAAAGAGTTCACATGGTGGAATACAAGAAGGCTGCGTACGCGTCAAGGCTAGCG
                                                       GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer
                                                                      GGCCTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCTGTCCCACCTGATCAACTTCC
                                                                                                                                                                   LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly
                                                                                                                                                                                   AAGCATAGAGTTTTGGCTGACCCAACCAAGTCAAGGTTGTTGTACTTTGGAGGA
                                                                                                                                                                                                                          ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGluGluCys
                                                                                                                                                                                                                                                                                300 LeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla
 GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer
                  GGATTTGGAGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTAACAGCACCTCA
                                                                                                              PhePheIleAsnValGlyAsspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal
                                                                                                                                        TTTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGGGAGGTTTAAAAGTGTA
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1 (bases 1 to 1245)

1 (bases 1 to 1245)

1 (bases 1 to 1245)

1 (arcia-martinez, J.L. and Lopez-Diaz, I.

1 (beda-Tomas, S. Garcia-Martinez, J.L. and Lopez-Diaz, I.

1 (arcia-roman, and multi-site polyadenylation of the second and GA 2-oxidases in Nerium oleander
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Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                              1245 bp mRNA linear
Nerium oleander GA 2-oxidase 2 mRNA, complete cds.
AY594292
                                                                                                                                                                                                                                                                                                                                                     GATAATAGACTCGGCCCTTTTGAGAAATCTGCTGCT 1097
                                                                                                                                                                                                                                                                                                                                       AspAsnArgLeuAlaProPheGlnLysSerAlaAla 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1245
/organism="Nerium oleander"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nerium oleander (common oleander)
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(GA2ox3) mRNA, complete cds.
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Mukaryota, Virtdiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Gentianales, Apocynaceae, Apocynoideae,
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80
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 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
                   260 LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly
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                                                                                   555 ATTCATCCTAGGAACGTTTTCAGTAAACTTCTAATGGACGAAAAGAGTGACTCTGTTTTC
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                                                                                                                                                                                                                                                                                                                                     161 IleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLysSerAspSerCysPhe
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1 (bases 1 to 1406)
Ubeda-Tomas, S., Garcia-Martinez, J.L. and Lopez-Diaz, I.
1801ation, characterization and multi-site polyadenylation of GA 20-oxidases and GA 2-oxidases in Nerium Oleander
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Nerium oleander gibberellin 2 oxidase
AY588978
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AY588978
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CEEFGFFKVINHSVPTEFITKLESEAIKFFSSPLSEKQKAGPADPFGYGNKKIGPNGD
VGWVEYILLSTNSEFNYHKFASILGVNPETIRAAVNDYVSAVKKMACEILEMLABGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IHPRNVFSKLLMDEKSDSVFRLNHYPPCPEIQOFSDNNLIGFGEHTDPQIISVLRSNN
TSGLQILLKNGHWISVPPDPNSFFINVGDSLQVMTNGRFKSVRHRVLANSVKSRLSMI
YFGGPPLSEKIAPLASLMEGEESLYEEFTWFEYKKSAYKTRLADNRLVLFEKVAAS"
                                                                                                                                                                                                                                                                                                                                                               Sakane, M., Nakajima, M. and Yamaguchi, I.

Direct Submission

Submitted (28-CCT-2003) Masayuki Sakane, University of Tokyo,
Submitted (28-CCT-2003) Masayuki Sakane, University of Tokyo,
Supplied Biological Chemistry; Yayoi 1-1-1, Bunkyo-ku, Tokyo
113-0032, Japan (B-mail:m-sakane@pgrl.ch.a.u-cokyo.ac.jp,
URL:http://pgrl.ch.a.u-tokyo.ac.jp/, Tel:81-3-5841-5158(ex.25158),
Fax:81-3-5841-8025)
                                                                                                                                                                                               Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Bukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicotyledons,
asterids, lamiids, Solanales; Solanaceae, Nicotiana.
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213
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2
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/db_xref="G1:46849529"
320 AspAsnArgleuAlaProPheGlnLysSerAlaAla 331
                                                                                                                                                                                                                                                                                                  Sakane, M., Nakajima, M. and Yamaguchi, I.
Molecular cloning of GA 2-oxidase in BY-2
Upublished
2 (bases 1 to 1292)
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Matches:
Conservative:
Mismatches:
Indels:
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/db_xref="taxon:4097"
/cell_line="BY-2"
1. .1292
/gene="GA2ox1"
75. .1073
                 Gaps:
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Best Local Similarity:
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MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J., Gaskin, P., Lange, T. and Hedden, P. Gibberellin Al2-aldehyde in endosperm and embryos of Marah macrocarpus Plant Physiol. 113 (4), 1369-1377 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLN 01-MAY-1997
                                                                                                                                                                                                                                                                                                    SerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPhe 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marah macrocarpus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosida, eurosida I, Cucurbitales, Cucurbitaceae, Marah.
                                                                                                           118 TACTCCTTTTCATTAATGTTGGTGATTCCTTGCAGGAAATGACTAATGGGAGATTTAGG
                                                                                                                                                                                                                                                                                                                      278 GlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                    298 GluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                  898 GAAAGTTTGTATAAGGAATTCACATGGTGTGAATACAAGAAGTCAGCTTACAAGACGAGG
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                                                CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn---ArgAsn
                                                                                                                                                                         ThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGln
                                                                                                                                                                                                                                         238 ThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
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/organism="Marah macrocarpus"
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/dev_stage="immature seed"
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M.macrocarpa mRNA for dloxygenase.
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/codon start=1
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KACQEFGFFKVINHGVPLEFITKLEGEAVKFFNLPQPEKEKVRPAKFPGYGNKRIGQN
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NYSGLQISLKOGTWAVSVPPDQYSFPINVGDSLQVMTNGRFRSVKHRVFADGLKSRVSM
IYLGGPPLDEKIAPLSSLAMEEGEESLYKEFTWCEYKKSAYKTRLGDNRLKFFFEKSVGQ
                 2 (bases i to 1406)
Ubcada-Tomas, Garcia-Martinez,J.L. and Lopez-Diaz,I.
Ubcada-Tomas,S., Garcia-Martinez,J.L. and Lopez-Diaz,I.
Direct Submission
Submitted (02-APR-2004) Instituto de Biologia Molecular de Plantas,
CSIC/Universidad Politecnica de Valencia, Avda de los Naranjos sn,
Valencia 46022, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CCCTCCACCAACTTCTAGGAAGGAATTCCTGTGACACCTCTTCAAACCTGAGGGCAAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                  /product="gibberellin 2 oxidase"
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                                                                                                                             1. .1406

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1. .1406
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WISVPPDHSSFFINVGDSLQVMTNGRFKSVKHRVLTNSSKSRVSMIYFGGPPLSEKIA
                                                                                  976 GGCCACCTTTGAGTGAAAGATAGCCCCTTTACCTTCCCTAATG---AAAGGAGAAGAA 1032
                                                                                                                                    CMA315663 1383 bp mRNA linear PLN 19-JUN-2003
Cucurbita maxima partial mRNA for Gibberellin 2-oxidase (ga2ox
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frisse, A. and Lange, T. Gibberellin biosynthesis in young seedlings of Cucurbita maxima Unpublished
TU
GERMANY
                                                                                                                    299 CysleufyrlysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeu
                                                   GlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGlu
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4, D-38106 Braunschweig,
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Conservative:
Mismatches:
Indels:
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/cultivar="Riesenmelone, gelb ge
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1. .1383
                                                                                                                                                                                                                                                                                                                                   AJ315663
AJ315663.1 GI:32127336
Ga2Ox gener; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
Cucurbita maxima
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Submitted (19-JUN-2001) Lange
Braunschweig, Mendelssohnstr.
related entry AJ315662.
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/gene="ga2ox"
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                                                                                     60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer 79
        SerThrProLeuPheThrGly1leProValValAspLeuThrHisProAspAlaLysAsn
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AB031206 1292 bp mRNA linear PLN 28-JUL-2004 Lactuca sativa Ls2ox1 mRNA for gibberellin 2-oxidase No1, complete

cds. AB031206 AB031206.1 GI:9971226 gibberellin 2-oxidase Nol.

VERSION KEYWORDS

cdB

DEFINITION ACCESSION

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Lactuca sativa
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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                                                                                                                                                                                                                                                                        Toyomasu, T., Mitsuhashi, W. and Kamiya, Y.
Toyomasu, T., Mitsuhashi, W. and Kamiya, Y.
Direct Submission
Submitted (17-AUG-1999) Tomonobu Toyomasu, Yamagata University,
Faculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata
997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp,
Tel:81-235-28-2861, Fax:81-235-28-2812)
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Nakaminami, K., Sawada, Y., Suzuki, M., Kenmoku, H., Kawaide, H.,
Mitsuhashi, W., Sassa, T., Inoue, Y., Kamiya, Y. and Toyomasu, T.
Deactivation of gibberellin by 2-oxidation during germination
photoblastic lettuce seeds
Biosci. Biotechnol. Biochem. 67 (7), 1551-1558 (2003)
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Matches:
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                     /mol_type="mRNA"

cultivar="Riesenmelone, gelb gen
/db xref="texon:3661"
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1. 1308
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Matches:
Conservative:
Mismatches:
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Gaps:
  organism="Cucurbita maxima"
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Submitted (14-DEC-2000) Lange T., Botanical Institute, Dept. Plant
Physiology and Biochemistry, TU Braunschweig, Mendelsschnstr. 4,
Braunschweig, D-38106, GERMANY
Location/Qualifiers
1.1308
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                                                                                                                                                                                                                                                                                                               158 GlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAsp 177
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GlyProAsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVal
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Cucurbita maxima mRNA for gibberellin 2-oxidase (ga2ox gene)
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ga2Ox gene; gibberellin 2-oxidase.
Cucurbita maxima (winter squash)
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                        GlyValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPheLysLys
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Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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SerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThr
                                             TCTGGATTTCAAATCTCTCTCTGGAATGGGAATTGGATATCTGTTCCTCCCCGATCACAGC
                                                                                          TCCTTCTTCATCATGTTGGTGACTCTTTACAGGTGATGATGATGGAAGATTCAAAAGT
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 1350 28-FBB-2002;
The Scripps Research Institute (US) ; Syngenta Participations P(CR)
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/db_xref="taxon:3702"

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Ada57916 Arabidops
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Adm94205 Soybean G
Add70120 Rice gene
Add60081 Rice gene
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Adx60259 A. thalia
Adx60268 Maize gib
Adx60268 Arabidops
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      Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USFTO spool/US106704454/runat_27122005_124840_29089/app_query.fasta_1.519
-Q=/cgn2_1/USFTO spool/US106704454/runat_27122005_124840_29089/app_query.fasta_1.519
-DB=N_Geneseq -QFMT=fastap -SUFTX=p2n.rng -MINMÄTCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNTTS=bits -START=1 -END=-1 -MATRIX=bits -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UUTFMT=ptc - NORM==xt -HEARPSIZES=500 -MINLENE - MAXENN=200000000
-USER=US10670454_@CGN 11 727_@runat_27122005_124840_29089 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE_0 -DELXT=7
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Aaz99471 Soybean g
Aad40261 Soybean G
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Scoring table:

WPI; 2004-758349/74

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New DNA plasmid comprising a T-DNA comprising an Agrobacterium Ti plasmid first border region linked to a transgene linked to an Agrobacterium Ti plasmid second border region, useful for enhancing production of
                           transgenic plants.
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## Example 1; SEQ ID NO 3; 77pp; English.

The present invention relates to a DNA plasmid comprising a transfer DNA (T-DNA) comprising an Agrobacterium Ti plasmid first border region linked to at least one transgene linked to an Agrobacterium Ti plasmid second border region, and located in the DNA plasmid outside of the T-DNA is a plant expression cassette comprising a plant cell non-lethal negative selectable marker gene linked to a vector backbone DNA. Also disclosed are a method for enhancing the selection of transgenic plants that do not contain vector backbone DNA, a method for reducing the copy number of a transgene in a plant cell, and a transgenic plant produced by the method. The DNA plasmid comprises the expression cassette comprising a promoter that functions in plant cells operably linked to a plant cell non-lethal negative selection marker gene. The promoter is a constitutive promoter. CF The promoter sexpresses the linked non-lethal negative selection marker gene culture during plant regeneration. The plant cell non-lethal negative selectable marker gene comprises a plant positive selectable marker gene of signalling gene, or metabolic interference from antibiotic resistance and herbicide resistance. The plant hormone comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway gene or signalling gene, or metabolic interference comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway genes, auxin pathway gene, ethylene pathway genes, cytokinin pathway genes, auxin pathway gene, ethylene pathway genes, comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway genes, auxin pathway genes, thylene pathway genes, comprises a transgene of agronomic interest. The plant hormone biosynthetic pathway genes, auxin pathway genes, thylene pathway genes, comprises a transgene of agronomic interest. The plant of pathway genes a transgene of genes, auxin pathway genes, ethylene pathway genes a comprise seal cransgenic plants. The sequence represents bequence represents bequence is

## Sequence 999 BP; 263 A; 221 C; 249 G; 266 T; 0 U; 0 Other;

999 331 0 0 0		PheLeuLysProPheLysSer 20	TICCTICTGAAACCATTCAAGICC 60	ThrHisProAspAlaLysAsnLeu 40	ACGCACCCCGATGCCAAGAATCTC 120	LeuValAsnHisGlyValProLeu 60	CTIGIGAACCAIGGIGITCCAIIG 180	PhePheLysLysSerGlnSerGlu 80	TICTITAAAAATCICAGICCGAG 240	yrGlySerLysArgIleGlyProAsn 100	GGTAGCAAGAGGATTGGCCCAAAC 300	ThrAsnProAspVallleSerPro 120	ACCAACCCTGATGTTATCTCACCC 360
2.61e-180 Length: 10.48.00 Marches: 100.00\$ Conservative 100.00\$ Mismatches: 100.00\$ Indels:	x ADT62692 (1-999)	MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuI	AIGGTTGTTCTGTCTCAGCCAGCATTGAACCAGTTTTTCCTTCTGAAACCATTCAAGTCC	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu	ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACCTCACGCACCCCGATGCCAAGAATCTC	IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTAACCATGGTGTTCCATTG	GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysEserG		LysAspArgAlaGlyProProAspProPheGlyTyrC	AAAGACAGAGCTGGTCCCCCCGACCTTTCGGCTATGGTAGCAAGAGGATTGGCCAAAC	VTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVall1	GGTGATGTCGGTTGGGTCGATACCTCCTCTCTCTAACACCCTGATGTTATCTCACCC
: ity:	(1-331)	MetValValLe	ATGGTTGTTC	ThrProLeuP	ACGCCCTTGT	IleValAsnA]	ATAGTGAACG	GluLeuMetA	GAGTTAATGG	LysAspArgA	AAAGACAGAGG	GlyAspValGl	GGTGATGTCG
ent S No.: t Sim ocal Match	US-10-670-454-2	П	Н	21	61	41	121	61	181	81	241	101	301
Alignment Pred. No.: Score: Percent Si Best Local Query Matc	US-10-	ò	qq	ò	Dp	δ	qq	ઠે	qq	à	qq	ò	<u>අ</u>

ò	121	Lysse	LysserLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr	140
ΩD	361	AAATC		420
ò	141	IleTh:	IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly	160
qq	421	ATTAC		480
ò	161	11eArg	leArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe 1	180
Ωp	481	ATAAG		540
à	181	Argle	ArgueuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly 2	200
qq	541	AGGTT		600
ð i	0	PheG1	PheGlyGluHisThrAspProGln1le1leSerValLeuArgSerAsnSerThrSerGly 2	21 (
g G	601	TTTGG		9
ζ	221	Leugl	LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe 2	4,
QD	661	TTGCA		720
ò	241	Phe11	PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLy8SerValLys 2	9
q	721	TTCAT		780
<i>8</i> €	261	Hisark	HighrgValLeuhlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyPro 2 	280
3		5		, ,
λo	œ	AlaLe 	AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu 3	0
đ C	841	GCGTT		900
λ	0	Tyrty	TyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAsp 3	N
QΩ	901	TACAA	screceracacricaaecraecrear	960
ò	321	AsnArg	AsnArgLeuAlaProPheGlnLysSerAlaAla 331	
qq	196	AATAG	66	
RESUI AAZSI ID	2 .2 .255912	standa	ard; cDNA; 1318 BP.	
¥ 2;	AAZ55912;			
<b>4</b> 51	10-APR-20	00	(first entry)	
3 E S	Runner be	an gibbe	bberellin 2-oxidase PcGA2ox1 cDNA.	
<b>X &amp; &amp;</b> )	bberell	in 2 ion;	-oxidase; PcGA2ox1; runner bean; 2-beta-hydroxylation; growth inhibition; 88.	
\$8\$	aseolus	Ü	neus.	
######## #############################	<u>γ</u> .α		<pre>Location/Qualifiers 681066 /*tag= a /product= "Gibberellin 2-oxidase PcGA2ox1" /transl_except= (pos:10581063, aa:Ala)</pre>	
\$ Z. \$	WO9966029	-A2.		
<b>₹</b> £\$		o		
PF	11-JUN-19	166	99WO-GB001857.	
. K K	12-JUN-19 15-JUL-19	98;	98GB-00012821. 98GB-00015404.	

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This sequence represents cDNA encoding a runner bean gibberellin (GA) 2-
cxidase, PcGA2cx1. This enzyme is a GA 2-beta-hydroxylase that acts on
CC cy19-GAs and for which 2-beta-hydroxylation is its only activity.
CHYGTCXYlation at the 2-beta-hydroxylation of a GA results in a biologically
inactive product, and is the most important route for GA metabolism in
CC plants, ensuring that the active hormones do not accumulate in plant
CC gibberellin 2-oxidase can be constitutively over-expressed or otherwise
CC enhanced to reduce the concentration of bloactive GAs in the plants and
CL therefore to inhibit plant growth of Encettive GAs in the plants and
CL therefore to inhibit plant growth agricultural and horticultural applications such as enhancing lodging-
CC resistance and grain yield in cereals, improving seedling quality,
C reducing the growth of amenity grasses, reducing shoot growth in orchard
and ornamental trees, improving tolerance to cold, drought and infection,
CC and increasing yields (by the diversion of assimilates from vegetative to
C and increasing yields (by the diversion of assimilates from vegetative to
C reproductive organs). The nucleic acids may also be used to induce male
CC and increasing yields the diversion in floral organs), prevent pre-
CC harvest sprouting, reduce shoot growth in hedging plants, inhibit
C reversibility in the development or germination of seeds and reduce shoot
C growth in commercial wood species. Antisense constructs of the nucleic
CC acids can also be used to transform plants to reduce the expression of GA
C 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
CC acids can also be used to transform plants to reduce the expression of GA
C 2-oxidase (claimed) to promote plant growth, (e.g., to improve fruit set
CC and growth in seedless grapes, increase stem length and rhurefore
C imcrease growth in woody species
C increase growth in woody species
                                                                                                                                                                                                                d plant gibberellin 2-oxidase enzymes and nucleic acids, used transgenic plants with improved or altered growth
                                                                              Phillips AL;
                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 42pp; English.
                                                                            Hedden P,
                            (UYBR-) UNIV BRISTOL
                                                                                                                                 WPI; 2000-097742/08
P-PSDB; AAY58597.
                                                                                                                                                                                                                New isolated plant
                                                                                                                                                                                                                                            to produce trans
characteristics.
                                                                              Thomas SG,
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Sequence 1318 BP; 358 A; 296 C; 282 G; 382 T; 0 U; 0 Other;

Alignm Pred.	Alignment Scores:	res:	3.896-180	Length:	1318
Score:			1748.00	Matches:	331
Percen	Percent Similarity:	arity	100.00%	Conservative:	0.0
Best L Ouery	Best Local Sım Query Match:	Best Local Similarity: Query Match:	100.00%	Mismatches: Indels:	00
DB:			3	Gaps:	0
US-10-	670-454	-2 (1-331)	US-10-670-454-2 (1-331) x AAZ55912 (1-1318)	1318)	
ò	н	MetValVal	LeuSerGlnProAla	LeuAsnGlnPhePhei	MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
qa	69		CTGTCTCAGCCAGCA	TTGAACCAGTTTTTC	
ò	21		PheThrGly1lePro	ValvalAspLeuThr	ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu 40
qq	128		TTCACGGGGATTCCT	GTGGTCGACCTCACG	ACGCCCTTGTTCACGGGGATTCCTGTGGTCGACGCACCCCGATGCCAAGAATCTC 187
ò	41		AlaCysArgAspPhe	GlyPhePheLysLeu\	leValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
qq	188		GCCTGTAGGGACTTC	GGCTTCTTCAAGCTTC	ATAGTGAACGCCTGTAGGGACTTCGGCTTCTTCAAGCTTGTGAACCATGGTGTTCCATTG 247
ò	61		AlaAsnLeuGluAsn	GluAlaLeuArgPhel	GluLeuMetalaAsnLeuGluAsnGluAlaLeuArgPheLysLysSysSerGlnSerGlu 80
QQ	248		GCCAATTTAGAAAAC	GAGGCCCTCAGGTTC	GAGTTAATGGCCAATTTAGAAAACGAGGCCCTCAGGTTCTTTAAAAAATCTCAGTCCGAG 307
ò	81		AlaGlyProProAsp	ProPheGlyTyrGly	LysaspargalaglyproproaspProPheGlyTyrGlySerLysarg11eGlyProAsn 100
a	308		GCTGGTCCCCCCGAC	CCTTTCGGCTATGGT	AAAGACAGAGCTGGTCCCCCCGACCCTTTCGGCTATGGTAGCAAGAGGATTGGCCCAAAC 367

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                                                                                                                                                PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhely8SerValLy8
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                                               LysSerbeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
                                                                                                IleThralaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly
                                                                                                             LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
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GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVallleSerPro
                                                                       428 AAATCACTITIGCATITITICCGAGAAAATCCTCATCATITICAGGGGGGGGTGGAGAACTAC
                                                                                                                                                                                                 ArgleuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
                                                                                                                                                                                                                 PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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                        368 GGTGATGTCGGTTGGGTCGAATACCTCCTCAACACACCAACCCTGATGTTATCTCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product = "gibberellic acid 2-oxidase 1"
/trans except = (pos: 633. .635, aa: Xaa)
/note = "Xaa is an unspecified amino acid"
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942 CCACCCTTGTGTGAAAAGATAGCACCTTTACCTTCACTCATGTAAAAGGAGAAGAAGT 1001
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402 GGCGATGTCGGTTGGGTCGAATACCTCCTTCTCAACACCAACCTGATGTCATCTCCCCC 461
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                                            121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
                                                                                    462 AAGTCACAGTTCATTTTCAGAGAAGGTCCTCAGAATTTCAGGGGGGGTGGTGGAGGAATAC
                                                                                                                                                      522 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGAGGGATTGGGG
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/*tag= a
/product= "GA 2-oxidase 1 protein"
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/note= "Xaa = any amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a gibberellic acid 2-oxidase 1 protein describes methods is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-xidase, phytoene synthase, C-20 oxidase, and a 2beta, abata-hydroxylase polymucleotides to achieve this. The method is used to control seed genenination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 ATGGTTGTTCTGTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAGCCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 ATAGTCAATGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCGTTA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 CAGTTCATGGCCAATTTGGAAAACGAAACCCTCGGGTTCTTCAAAAAACCTCAATCCGAG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       342 AAAGACAGGGCTGGTCCCCCTGACCCTTTTGGCTACGGCAGCAAGAGGATTGGCCCTAAC 401
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                                                                                                                                                                                                                                      Kishore GM, Logusch EW, Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                               Obtaining tranagenic plant useful for controlling seed germination ar seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 45; Page 248; 267pp; English
                                                                                                                                                                                                                                      Heck GR,
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87.56%
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99US-0137977P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compared to normal plants
                                                                                                                                                                                                                                   Brown SM, Elich TD,
Piller KJ, Rao S, F
                                                                                                                                                                                            (MONS ) MONSANTO CO
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Query Match:
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WO200009722-A2
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                                                                                    10-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                     ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 LeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAla
                                                                                                            IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe
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                         522 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGAGGGATTGGGG
                                                                                 582 ATAACGCAGAGGAATGTGTTGAGTAGGTTGCTGAAGGATGAGAAGAGGTGATYCTTGCTTC
                                                                                                                                                                        GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer
                                                                                                                                                                                                                               GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana; plant; gene; stress; transgenic; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspAsnArgLeuAlaProPheGlnLysSerAlaAla
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                      The invention relates to control of gibberellin (GA) levels in plants.

The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increased uniformity of germination, emergence consistence in a slee useful in storage and transport of seeds to reduce premature germination which may affect agronomic or food quality of the seeds. The present sequence is soybean GA 2-oxidase 1 cDNA
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                                                                                                                                                         Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer
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                                                                       Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1359 BP; 340 A; 305 C; 304 G; 409 T; 0 U; 1 Other;
                                                                       Logusch EW,
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Matches:
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Mismatches:
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                                                                     Kishore GM,
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                                                                       Heck GR,
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                                                                     Elich TD,
                                                                                      Rao S,
                                                                                                               2002-489107/52
                                           (BROW/) BROWN S M.
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Best Local Similarity:
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                                                                                   Piller KJ,
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                                          cell has been exposed, comprising: (a) contacting nucleic acid array or probes representative of the plant cell with an array or probes representative of the plant cell genome, and (b) detecting a profile of expressed polynucleotides in the plant cell with an characteristic of a stress response. The method is useful in the production of transgenic plants. Cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                    121 GCGAAAACCCGAATCGTAAAAGCCTGCGAGGAGTTCGGGTTCTTCAAGGTCGTAAACCAC 180
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                                    invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                       MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
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            + Sequence Listing; English
                                                                                                                                                                                           Sequence 1026 BP; 274 A; 242 C; 251 G; 259 T; 0 U; 0 Other;
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Mismatches:
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
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LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr
                                                                                                                                                                                                    778 AAGAGTGTTAAACACAGGGTCTTAGCCGATACAAGGAGGATCGAGGATTTCAATGATATAT
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                                                                         GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArqPhe
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Whitham S,
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illustrate the invention.
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F, Quan S,
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This sequence represents CDNA encoding an Arabidopsis thaliana

CC gibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-

CC dibberellin (GA) 2-oxidase, PcGA20x2. This enzyme is a GA 2-beta-

CC dibberellin (GA) 2-oxidase, profact, and is the most important route for

its only activity. Hydroxylation at the 2-beta position of a GA results

CC Am entabolism in plants, ensuring that the active hormones do not

CC GA metabolism in plants, ensuring that the active hormones do not

CC commulate in plant tissues. The nucleic acids can be used to transform

CC accumulate in plant tissues. The nucleic acids can be used to transform

CC contemplate of reduce the concentration of bloactive GAS in the

CC or otherwise enhanced to reduce the concentration of bloactive GAS in the

CC plants and therefore to inhibit plant growth. Growth inhibition is useful

CC plants and infereasing yield in Cereals, improving seedling

CC lodging-resistence and grain yield in Cereals, improving seedling

CC quality, reducing the growth of amenity grasses, reducing shoot growth in

CC corchard and onnamental trees, improving tolerance to cold, drought and

CC infection, and increasing yields (by the diversion of assimilates from

CC corchard and ornamental trees, improving tolerance to cold, drought and

CC infection, and increasing yields (by the diversion in floral organs),

CC inhibit reversibility in the development or gerwintation of seeds and

CC reduce shoot growth in commercial wood species. Antisense constructs of

CC inhibit reversibility in the development or gerwintation of geeds and

CC reduce shoot growth in commercial wood species. Antisense

CC improve skin texture and fruit shape in apples, increase stem

CC length and therefore yield in sugar cane, increase stem

CC length and therefore yield in sugar cane, increase stem

CC length and therefore yield in sugar cane, increase growth in woody species

CE CASTANT AND CONTRACT AND CONTRAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated plant gibberellin 2-oxidase enzymes and nucleic acids, used to produce transgenic plants with improved or altered growth characteristics.
                                                                                                                                                                                                                                                                                                      Gibberellin 2-oxidase; AtGA2ox2; 2-beta-hydroxylation; inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Gibberellin 2-oxidase AtGA2ox2"
                                                                                                                                                                                                                                                           Arabidopsis thaliana gibberellin 2-oxidase AtGA2ox2 cDNA
317 ArgleuAlaAspAsnArgleuAlaProPheGlnLys 328
                      Location/Qualifiers
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98GB-00015404.
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                                                                                                                                                                                                                                                                                                                          growth inhibition; ss.
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                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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99US-0143401P.
99US-0143412P.
99US-0146650P.
99US-0170906P.
99US-0172946P.
                                                                                                                                            ADM94213 standard; cDNA; 1352
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                                                                                                                                                                                                                              Soybean Dioxygenase cDNA #2.
                                                                                                                                                                                                   (first entry)
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Lohman KN, Rer
, Zoughi IL, A
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(PION-) PIONEER
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12-JUL-1999;
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Shen JB,
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297
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                                                                                                                                                                                     MetValValLeuSerGlnProAlaLeu-----AsnGlnPhePheLeuLeuLysProPhe 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                826 CACTCTTCTTTCTTTAATGTTGGAGATGCTCTTCAGGTTATGACTAACGGGAGGTTC
                                                                                                                                                                                                                                              LysSerThrProLeuPheThr-----GlyIleProValValAspLeuThrHisProAsp
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                                                                                                                                                                                                                                                                                                       AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis
              280 G; 324 T; 0 U; 0 Other;
                                                       1237
210
45
72
5
                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                               Indels:
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              BP; 356 A; 277 C;
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1092.50
76.81%
63.25%
62.50%
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Best Local Similarity:
              Sequence 1237
                                           Alignment Scores:
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1006 GATGATTGGCTTTACAAAGAATTCACTTGGTCTCAATACAAATCTTCTGCTTACAAGTCT 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSer 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I, Rafalski JA, Orozco EM, Miao G, Famodu OO;
Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                                                                                                                                            Soybean; ss; plant; plant metabolism; GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase; Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase; Gaclosterene Structurene Synthase A; GA-20 oxidase; Ethylene response factor; Acyl-CoA thioesterase II; Pagroproter GTOX20-like; P-91ycoprotein I; P-91ycoprotein 3; P-91ycoprotein AFPGP; P-91ycoprotein HVMDR2; AGC transporter; PP-91ycoprotein AFPGP; P-91ycoprotein HVMDR2; AGC transporter;
                                                                                                         317 ArgleuAlaAspAsnArgleuAlaProPheGlnLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; SEQ ID NO 13; 186pp; English
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HI-BRED INT INC.
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3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response factor, Acyl-CoA thioesterase II, ABC transporter GCN20-like, P-GA thioesterase II, ABC transporter GCN20-like, P-GA transporter.

Sylvoprotein I, P-GJYCOPTOTEN ABC transporter and MRP4 ABC transporter.

HYMDR2, ABC transporter, PMP10 ABC transporter and MRP4 ABC transporter.

The nucleic acid fragments may be used to create transgenic plants where the polypeptides are present at higher or lower levels than normal or in cell types or in developmental stages in which they are not normally found. The polynucleotides can be used as probes for genetically and plysically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length polymorphism (RFLP). It can also be used to probe Southern blots containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross.

The nucleic acid fragments may also be used trom the mutation probbes against PCR amplification products generated from the mutation problation using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or produce polyclonal or monoclonal attuin cells or in vitro in cell for detecting the polypeptides in altu in cells or in vitro in cell cextracts. The present sequence encodes a plant metabolism protein (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment).
              $$$$$$$$$$$$$$$$$$$$$$$$$$$
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## Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other;

200	Sequence 1352 BP; 439 A; 255 C; 243 G; 415 T; 0 U; 0 Other	Other;
Alignment Pred. No.: Score:	4.53e-106 Length: 1068.50 Matches:	
Percen Best L Query	t Similarity: 77.95% ocal Similarity: 60.73% Match: 61.13%	
DB:	12 Gaps: x ADM94213 (1-1352)	
i B	1 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLygProPheLygSer	uLysProPheLysSer 20
Ωp	:::      ::: 159 ATGGTGTTGTTGTCCAAAGCAACAACAACAATACTCCTACATTAAGAACTGCATGCCA	:     TAAGAACTGCATGCCA 218
È	21 ThrProLeuPheThrGlylleProValValAspLeuThrHisProAspAlaLysAsnLeu	oAspAlaLysAsnLeu 40
дg	219 ACCAAATTTCCTCAACAATTCCCATAGTGGACCTCTCCCAAACCTGATGCAAAGACCCTT	TGATGCAAAGACCCTT 278
ò	41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu	nHisGlyValProLeu 60
qa	279 ATAGTGAAGGCTTGTGAGGAGTTTGGATTCTTCAAAGTCATCAA	TCATGGTGTCTCCATG 338
È	61 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu	sLysSerGlnSerGlu 80
QQ	339 GAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTC	TATGICACTCAATGAA 398
ò	81 LygAgpArgAlaGlyProProAspProPheGlyTyrGlySerLygArglleGlyProAsn	sArgileGlyProAsn 100
οp	399 AAGGAAAAGTAGGACCTCCCAATCCATTTGGGTATGGTAGGA	GAAAATTGGACACAAT 458
ò	101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro	oAspValIleSerPro 120
Op	459 GGGGACGTTGGATTGAGTACCTTCTTCTTCAACACCAATCA	AGAA 506
ò	121 LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr	aValValGluAsnTyr 140
qq	507 CACAACTICICIGITIAIGGGAAAAACCCIGAGAAATICAGGIC	TCTGTTGAACAGTTAC 566
ò	141 IleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160	tAlaGluGlyLeuGly 160
qq	567 ATGTCTTCTGTGAGGAAGATGGCATGTGAGATTCTTGAGTTGT	GCCAGAAGGCTTGAAG 626
ò	161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe	sSerAspSerCysPhe 180
qq	627 ATTCAGCAAAAGGATGTGTTTAGCAAGCTTCTAATGGATAAACA	AAGTGACTCTATTTTC 686
ò	181 ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly	nArgAsnLeuValGly 200

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987 CCTTTGAGTGAGAAAATAGCACCATTATCCTCTCATG---AAAGGAAAAGAAAGTTA 1043
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Lohman KN, Rendina AR, Sakai H, Weng Z, Caimi PG, Fang Y;
Zoughi II, Anderson SL, Shi J, Lu G, Helentjaris TG;
                                                                                                                                                                                                                                                               PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys
                                                                                                                                                                                                                                                                                                 TTTATTAACGTTGGTGATTCTCTTCAGGTTATGACAAATGGAAGGTTCCGAAGTGTGAGA
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                                                                                   TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAACAACACTTCAGGC
                                                                                                                                                        LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
                                                                                                                                                                                    281 AlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu
                                                       PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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PIONEER HI-BRED INT INC.
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99US-0143412P.
99US-0146650P.
99US-0170906P.
99US-0172946P.
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21-DEC-1999;
21-DEC-1999;
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30-JUL-1999;
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LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100

81

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New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
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P-PSDB; ADM94206

The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase incleotide sequence encoding a polypeptide having GTP cyclohydrolase [1/3,4-dihydroxy-2-butanone-4-phosphate synthase activity, appearing a coll with the comprising the polynucleotide operably linked to at least one regulatory sequence, transforming a cell with the polynucleotide a cell comprising the recombinant DNA construct.

The comprising the recombinant DNA construct and a seed comprising the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid consent and assembled contigs encoding plant metabolism proteins chosen from GTP cyclohydrolase (11/3,4-dihydroxy-2-butanone-4-phosphate (ECC (CDNA)) fragments and assembled contigs encoding plant metabolism proteins chosen from GTP cyclohydrolase (11/3,4-dihydroxy-2-butanone-4-phosphate (ECC (CDNA) thicesterase [11,360 transporter GC (GDNA) thicesterase are present at higher or lower levels than normal or in developmental stages in which they are not normally cell types or in developmental stages in which they are not normally collypseticals are present at higher or lower level as restriction fragment and progeny of a defined genetic cross containing restriction endomoleas Example 3; SEQ ID NO 5; 186pp; English fragment)

Sequence 1365 BP; 448 A; 258 C; 244 G; 415 T; 0 U; 0 Other;

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346 GAAGCTATATCCGAATTGGAATATGAAGCCTTCAAATTCTTCTTCTATGTCACTCAATGAA 405
                                                                                                             MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
                                                                                                                                                                                                           41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 60
                                                                                                                                                                                                                                                         GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu 80
                                                                                                                           Thr ProLeu Phe Thr Glylle ProVal Val Aspleu Thr His ProAspAlaLys AsnLeu
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200
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                          Conservative:
Mismatches:
Indels:
   Length:
Matches:
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3.42e-105
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60.42%
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994 CCTTTGAGTGAGAAAATAGCACCATTATCCTCTCATG---AAAGGAAAGAAAGTTG 1050
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                                    101 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
                                                                                    121 LysserLeuCysllePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
                                                                                                                                     IleThrAlaValLy8AsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160
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ArgieuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
                                                                                                                                                                                                                                                                                                                                                   IleargGlnargasnThrLeuSerargLeuLysasspGluLysSerAspSerCysPhe
                                                                                                                                                                                                                                                                                      PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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                                                  466 AGGGACGTTGGTTGAGTATGAGTACCTTCTTCTCAACACCAATCAAGAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "gibberellic acid 2-oxidase 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soybean gibberellic acid 2-oxidase 2 cDNA sequence.
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449 GGGGATGTTGGGTTGGGTTGAGTACCTTCTTCTCAACACCAATCAAGAA-
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/product= "GA 2-oxidase 2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a gibberellic acid 2-oxidase 2 protein sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels gibberellic acid levels methods for the inhibition and controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthetic pathway sequence, diverts subpresses the gibberellin biosynthetic pathway substrates or products. The methods uses copally diphosphate synthase, 3beta-hydroxylase, coxidase, phytoene synthase, C.20 oxidase, and a 2beta, 3beta-hydroxylase polynuclectides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of germination, in transgenic plants. The plants produced are gibberellin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||||||||:::||||||||:::
ATGGTGTTGCTGTCCAAGGCAACAACAACAATACTCCTACATCAAGAACTACATGCCA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                                                                                                                                                                                                                                                                                          Heck GR,
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Rao S, F
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Percent Similarity:
                                                                                                                                      10-AUG-1999;
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Piller
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                                                                                                                                                                                                                                                                                                                                          The invention relates to control of gibberellin (GA) levels in plants.

The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce the present sequence is soybean GA 2-oxidase 2 cDNA seeds. The present sequence is soybean GA 2-oxidase 2 cDNA
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                                                                                                                                                                                                    Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||||:::||||||||:::
| ATGGTGTTGCTGTCCAAGGCAACAACAATACTCCTACTTCAAGAACTACATGCCA
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                                                                                Logusch EW, Logusch SJ;
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                                                                                Elich TD,
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                                                                                                                                                                                   PhelleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICATAAATGTTGGTGATTCTCTTCAGGTTATGACCAATGGAAGGTTTCGAAGTGTGAAA
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                                                                                                 TTTGGAGAACACACGGACCCACAAATCATTCTCTACTTAGGTCCAACAATACTTCAGGC
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                                                                                                                                                         ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGly
                                                                                                                                                                                                                                                    PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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                                                                     IleargGlnargasnThrLeuSerargLeuLysaspGluLysSeraspSerCysPhe
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Zhu T,
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Whitham S, Xie Z,
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Katagiri F, Quan S,
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The invention relates to a DNA encoding a plant protein having applerellin 2-oxidation activity, comprising ADK000079 or ADK00081 or a DNA encoding a protein comprising ADK000800. ADK00082, where one or more amino acid residues are substituted, deleted, added, and/or inserted or DNA hybridising to ADK00079 or ADK00081 under stringent conditions. The DNA is also selected from an antisense RNA, a DNA encoding an RNA having the ribozyme activity that specifically cleaves the transcript of the DNA above, a DNA encoding an RNA that suppresses the expression of the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA encoding plant-derived proteins having gibberellin 2-oxidation activity, useful for the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression
                                                                                                                                             TACTTTGGAGGCCACCGTTAGCACAGAGGTTGCACCATTGCCACAGCTGCTGGGGAG
                                                                                                                                                                                                    TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys
                                                                                                                                                                                     GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThr
                            AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg
                                                                     PhelysSerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice, 88; gene; plant; gibberellin 2-oxidase; OsGA20x3; plant growth; gibberellin A20; gibberellin A29; gibberellin A29
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                                                                                                                                                                                                                                            SerArgleuAlaAspAsnArgleuAlaProPheGlnLys 328
                                                                                                                                                                                                                                                            Rice cDNA encoding gbiberellin 2-oxidase, OsGA2ox3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NAAG-) NAT INST AGROBIOLOGICAL SCI.
(BIOO-) BIO-ORIENTED TECHNOLOGY RES ADVANCEMENT.
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                                                     involved in plant resistance or response to pathogenic infection. Mi comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. Mill is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ACGGACACGATGGACAAGGCCGAGGCCGTCAGGTTCTTCTCCCCAGACGCAGGCC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLys 175
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                                         present invention relates to a method (M1) for identifying
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Conservative:
Mismatches:
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illustrate the invention.
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Local Similarity:
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Sakamoto

above in plant cells via RNAi, or a DNA encoding an RNA that suppresses the expression of the DNA above in plant cells by co-suppression. Also included are a protein encoded by the DNA above, a vector harbouring a DNA selected above, a transformed plant cell harbouring the DNA above or the vector, a transgenic plant comprising the transformed plant cell or the vector, a transgenic plant comprising the transformed plant cell or the vector, a transgenic plant, a method of producing a transgenic plant, a method of suppressor comprising the DNA above as an active plant, a method of suppressing plant growth and a method of promoting plant growth. The gibberellin 2-oxidase catalyses the conversion of gibberellin A20 to gibberellin A29, which is further metabolised to gibberellin A29-catabolite. The DNAs are useful in the inactivation of plant gibberellins and plants whose gibberellin activity has been modified by regulating the expression of these DNAs. The present encodes gibberellin 2-oxidase, OsGA2ox3 sequence 8

Sequence 984 BP; 165 A; 311 C; 341 G; 167 T; 0 U; 0 Other;

984	190			12	٣
Length:	Matches:	Conservativ	Mismatches:	Indels:	Gaps:
7.33e-96	973.00	72.67\$	57.06%	55.66%	12
Alignment Scores: Pred. No.:		Percent Similarity:	imilarity:	Query Match:	DB:

US-10-670-454-2 (1-331) x ADK00081 (1-984)

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AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsn-------Pro 115
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ATGGTGGTTCTCGCTGGCCCGCCGGTCGATCACATCCCGCTGAGGTCGCCGGAC 60
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MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
                                                                                                             40 LeulleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValPro 59
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759
                                                                                                          275
                                                                                                                                                                        276 TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys 295
                                                                                                                                                                                        296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThr 315
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                                                             256 PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                              AspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArg
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ii J, Ishikawa
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to N, Sato K, Nagata T, Kawakami N, Yazaki J,
Kawai J;
                                                                                                                                                                                                                                                                                                 316 SerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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SEIBUTSUKEI TOKUTEI SANGYO GIJUTSU.
DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
ZH KOKUSAI KAGAKU SHINKO ZAIDAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived DNA sequence, SEQ ID 2929
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                                                                                                                                                                                                                                                                                                                                                                                            AEB67784 standard; DNA; 1271 BP
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transcriptional-regulatory regions. This polynucleotide represents a DNA sequence taken from a rice genome clone library for use in the invention. Note: This sequence is not shown in the specification. It has been retrieved from a sequence listing in electronic format from the Japanese Patent Office. The invention claims DNA sequences of SEQ ID Nos 1 to however, the sequence listing only provided the DNA sequences of SEQ ID Nos 1 to Nos 1 to 3032.
                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                          MetValValLeuSer---GlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLys 19
                                                                                                                                                                                                                                                                                                                              20 SerThrProLeuPheThrGlylleProValValAspLeuThrHisProAspAlaLysAsn 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                   60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluLysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyPro
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52
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Matches:
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970 TACTITGGAGGCCACCGTTAGCACAGAGGATTGCACACTTGCCACAGCTGCTGGGGAG 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase nucleic acid and proteins, useful for creating transgenic plants where polypeptides are present at higher or lower levels.
                                                           295
                                                                                                                      GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThr 315
                            969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having GTP cyclohydrolase 11/3,4-dinydroxy-2-butanone-4-phosphate synthase activity, appearing as ADM94266. Also included are a vector comprising the polynucleotide, a recombinant DNA construct comprising the polynucleotide operably linked to at least one regulatory sequence, transforming a cell with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Orozco EM, Miao G, Famodu OO;
ai H, Weng Z, Caimi PG, Fang Y;
shi J. Lu G, Helentjaris TG;
                                                           TyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLys
                   PhelysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                                                                                                                                                                                                                                                                                                                                                                                Rice; 88; plant; plant metabolism;
GTP cyclohydrolase II/3,4-dihydroxy-2-butanone-4-phosphate synthase;
Dioxygenase; Ent-Kaurene Synthase A; GA-20 oxidase;
Gibberellin 3-beta hydroxylase; Riboflavin specific deaminase;
Ethylene response factor; Acyl-CoA thioesterase II;
ABC transporter GGN20-1ike; Peglycoprotein I; P-glycoprotein 3;
P-glycoprotein ATPGF; P-glycoprotein HVMNR2; AGC transporter;
PMP70 ABC transporter;
                                                                                                                                                                                                             1090 rcaacecriceacaacaacaacaccccacrircacaaac 1128
                                                                                                                                                                                  SerArgieuAlaAspAsnArgieuAlaProPheGlnLys 328
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Rendina AR, Sakai H, Weng Z,
Anderson SL, Shi J, Lu G,
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99US-0143412P.
99US-0146650P.
99US-0170906P.
99US-0172946P.
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Lohman KN, Ren
, Zoughi IL, A
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21-DEC-1999;
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Shen JB,
Li CP;
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producing a plant (comprising transforming a plant cell with the producing a plant (comprising transforming a plant from the transformed plant cell), a plant comprising the recombinant DNA construct, Also disclosed as new are nucleic acid the recombinant DNA construct. Also disclosed as new are nucleic acid chosen from GTP cyclohydrolase II/3,4-dihydroxy-2-butenone-4-phosphate consent from GTP cyclohydrolase II/3,4-dihydroxy-2-butenone-4-phosphate cynthase, Dioxygenase, Ent-Kaurene Synthase, Gibberellin CC 3-beta hydroxylase, Riboflavin specific deaminase, Ethylene response factor, Acyl-Cob, thiosesterase II, ABC transporter GRADG-like, P-Glycoprotein I, P-Glycoprotein 3, P-Glycoprotein AFGF, P-Glycoprotein I, P-Glycoprotein 3, P-Glycoprotein AFGF, P-Glycoprotein I, P-Glycoprotein ABC transporter and MRP4 ABC transporter. The nucleic acid fragments are present at higher or lower levels than normally collicity and pypeptides are present at higher or lower levels than normally collicity and pypylacically mapping genes and as markers for traits linked to those genes. The nucleic acid fragments may be used as restriction fragment length collymorphism (RELP). It can also be used as restriction fragment length containing restriction endonuclease-treated genomic DNAs of a set of individuals representing parent and progeny of a defined genetic cross. The nucleic acid fragments may also be used as hybridisation probes against PCR amplification products generated from the mutation population using the mutation tag sequence primer; The peptidides can also be used to immuniae animals to produce anythy and produce anythy any produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using the mutation tag sequence primer in conjunction with an arbitrary genomic site primer. The peptides can also be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides or proteins comprising the amino acid sequences. Antibodies are useful for detecting the polypeptides in situ in cells or in vitro in cell extracts. The present sequence encodes a plant metabolism protein (or
        comprising the recombinant DNA construct
    polynucleotide, a cell
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Sequence 1650 BP; 353 A; 463 C; 476 G; 358 T; 0 U; 0 Other;

	1650	190	. 25	79	12	3
		Matches:			Indels:	Gaps:
	1.54e-95	973.00	72.67%	57.06%	55.66%	12
Alignment Scores:	Pred. No.:	Score:	t Similarity:	Best Local Similarity:	Query Match:	DB:

US-10-670-454-2 (1-331) x ADM94203 (1-1650)

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1007 GGAGAGCAGAGCCTGTACAAGGAGTTCACATGGGATGAGTACAAGAAGGCTGCCTACAAA 1066
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156 AlaGluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLysAspGluLys 175
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                                                           SerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsn
                                                                                                                                     296 GlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlahlaTyrThr
                             587 TCGGAGGGCTGGGCATTGCGCAGGCGGACGCGCTGAGCGCGCTGGTGACGCGCGAAGGG
                                                                                                                                                                                216 AsnSerThrSerGlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProPro
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                                                                                                                                                                                                                                                           GACCGCGACTCCTTCTTCGTCAACGTCGCGCACTCGTTGCAGGTTCTGACCAATGGGAGG
                                                                                                                                                                                                                                                                                                    256 PhelysSerVallysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
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HTC; GSLT CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1362)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, M., Cruaud, C., Quetler, F., Scarpelli, C., Schacher, V.,

Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNSOABSJ 1362 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH78ZH09 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
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2 (bases 1 to 1362)
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-MODBL=frame+ p2n.model -DEV=xlh
-MODBL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10670454/runat_27122005_124841_29111/app_query.fasta_1.519
-Q=/cgn2 1/USPTO_spool/US10670454/runat_27122005_124841_29111/app_query.fasta_1.519
-DB=EST -QFWT=fastap -SUFFTX=p2n.rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNTS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MX=100 -THR MIN=0 -ALIGN=15 -MODB=LOCAL
-UVSRP=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10670454 @CGN 1 1 5315 @runat_27122005 124841_29111 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRREADS=1 -XGARPOP=10 -XGARPEXT=0.5 -FGAPOP=6
-FGAPOR=7 -YGAPOP=10 -YGAPDXT=0.5 -DELOP=6 -DELEXT=7
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and is derived by analysis of the total score distribution.
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Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Walssenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 prime are assembled with Phrap.
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/plasmid="pCMVSPORT_6"
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Conservative:
Mismatches:
Indels:
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/clone="GSLTPGH78ZH09"
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Web: www.genoscope.cns.fr)
The sequences are based on single pass reads.
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Genoscope members carried out sequencing and annotation: Castelli V., Aury J.W., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFB7ZE01 of Flowers and buds of strain col-0 of Arabidopsis
256
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                                          819 CACTCTTCTTCTTCATTAATGTTGGAGATGCTCTTCAGGTTATGACTAACGGGAGGTTC
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237 GlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe
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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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(bases 1 to 1141)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                            942 TTCGGCGGACCGCCATTGAGCCAGAAGATCGCACCATTGCCATGCCCTGTCCCTGAGCAA 1001
                                                                                                                                          882 AAGAGTGTTAAACACAGGGTCTTAGCCGATACAAGGAGATCGAGGATTTCAATGATATAT
                                     PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuDroSerValMetLeuLysGly
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Direct Submission

Submitted (18-NoV-2003) Genoscope - Centre National de Sequencage :

Submitted (18-NoV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 BVRY codex - FRANCE (8-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

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Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Project, University of Submitted (25-APR-2002) Maize Mapping Direct Submitted (25-APR-2002) Marketing are interested in getting corresponding physical clones, these are publicly available from ZMDB and may be found by BLAST wearching at MSL, maizemap.org; ZMDB, www.zmdb.iastate.edu, TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nin.gov. When the source of the maize CDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMDB: www.zmdb.iastate.edu.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                          /notce="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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/clone_lib="Maize Mapping Project/DuPont Cornsensus
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                                                                                                                                                                       GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer 176
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
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Fang, Z., Morgante, M., Landewe, T., Fengler, K., Useche, F.,
Hanafey, M., Tingey, S., Chou, H., Wing, R., Soderlund, C. and Coe, E.H.
                    VallleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
                                        AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn
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Plant Physiol. 134 (4), 1317-1326 (2004)
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design c Overgo Probes
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Location/Qualifiers
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/clone="GSLTFB56ZG10"
/tissue_type="Flowers and bu-
/ecotype="Col-0"
/plasmid="pchysporr 6"
/complement(1. .1128)
/gene="At1g78440"
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/organism="Arabidopsis
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AL SUBMILLAG (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRV cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads

Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.

URGY INRA : Clepet C., Cabocce M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences) 5 prime and 3 prime are assembled with Phrap.

Length
Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cnsuaDMT
Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB56ZG10 of Flowers and buds of strain col-0 of Arabidopsis haliana (thale cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                 914 CCCTCCGACGCGACGCCTTCTTCGTTAACGTCGGCGACTCGTTGCAGGTGCTGACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                              934 TTCATCTACTTCGCGGGGCCGCCGCTGGGGCAGCGGATCGCGCCGCTGCCGCAGGTGCTG
                                           694 GGCTGCAGCACCACGGCCTTCGGCGAGCACACCGACCCGCAGATCATCTCCGTGCTCCGC
                                                                                                                                                                                                   ProProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsn
                                                                                                                                                                                                                                                                                                                                         GlyArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSer
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                    LysSerAspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeu
                                                                                                AsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 TyrThrSerArgleuAlaAspAsnArgleuAlaProPheGlnLys 328
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HTC; GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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CNSOADMT
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Solanum tuberosum (potato)
Solanum tuberosum
Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.

E [bases 1 to 893)
S Flinn, B., Rothwell, C., Sardana, R., Griffiths, R., Lague, M., De
Koeyer, D., Audy, P., Goyer, C., Li, X.-Q., Wang-Pruski, G. and Regan, S.
Generation of ESTs from late blight-challenged potato tubers
Lu fupublished (2005)
Contact: Barry Flinn
The Canadian Potato Genome Project - BioAtlantech
921 College Hill Rd, Fredericton, ON, E3B 629, CANADA
Email: bflinn@bioatlantech.nb.ca
Seq primer: T3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   893 bp mRNA linear EST 15-MAR-2005
50141.1 Late Blight-Challenged Tubers Solanum tuberosum cDNA clone
DNS89159
                                                                                                                                                                                                                                   LysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyr 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 VallleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaVal 136
                                                                                                                                                                                                        AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg
                                                                                                                                                           PheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGly
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TCTGATTACAGAAATTTGCATCGGTTTTTGGTGAAGCTGCAGAAAATTCAGGTGTATA
                                                                                     157 GluGlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSer
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                                                                    ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla
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/mol_type="mRNA"
/cultivar="Shepody"
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AJ803092 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
AJ8033092
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                                                   274
                                                                         IleTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
                                                                                                                                                                                                             Antirrhinum majus (snapdragon)
Antirrhinum majus
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, lamiids, Lamiales, Plantaginaceae, Antirrhineae,
                                                                                                                                           73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bey, M., Stueber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H., Saedler, H. and Zachgo, S. Antirrhium Petal Development and Characterization of Antirrhium Petal Development and Identification of Target Genes of the Class B MADS Box Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GCCTCTTCTGAAAAAGAGAAAACAGGGAACCCTGACCCTTTTGGCTATGGAAGTAAGAAA
CCGGATCACACTTCCTTCTTCAACGTTGGTGACTCTCTCCAGGTGATGACAAATGGG
                                                     ArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMet
                                                                                                                                                                                             LysGlyGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                   968 AACTCTAGATTGTCTGATAATAGGCTTCAACAATTCGAAAGG 1009
                                                                                                                                                                                                                                                                 315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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Mismatches:
Indels:
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Molekulare Pflanzengenerik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers

    .785
    /organism="Antirrhinum majus"

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Plant Cell 16 (12), 3197-3215 (2004)
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902.50
81.30%
68.70%
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Best Local Similari
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                     728
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B1935635 tomato flower, anthesis Lycopersicon esculentum cDNA clone cTOD23D23 5' end, mRNA sequence.
ThrTrpCysGluTyrLysLysAlaAlaTyrThrSerArgLeuAlaAspAsnArgLeuAla 324
                                    663 ACATGGTTTGAGTACAAAATTCAGCATATAAATCTAGATTGGCTGATAATAGGTTGGTC 722
                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum Walthaman Subryophyta; Embryophyta; Tracheophyta; Subraryora; Viridiplantae; Streptophyta; Embryophyta; Core eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="anthesis"
/clone lib="tomato flower, anthesis"
/clone lib="tomato flower, anthesis"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
Xhoī; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases to 792) to 792) to 792) to 792) wan der Hoeven, R.S., Bezzerides, J.L., Karamycheva, S.A., Tsai, J., Utterback, T., Van Aken, S., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, anthesis (2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.ganome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLysProPheLysSer
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1158
42
156
2
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1.792
/organism="Lycopersicon esculentum"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  db_xref="taxon:4081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/cultivar="TA496"
                                                                                                                                                                                                                                                                      BI935635.1 GI:16250107
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723 CTATTTGAGAA 734
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Pred. No.:
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VERSION
KEYWORDS
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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                                                                              8
                                                      /clone libe "Late Older Blight-Challenged Tubers"
//clone libe "Late Older Blight-Challenged Tubers"
//note="Vector: pBluescript II SK(+) XR; Site I: EcoRI;
Site 2: XhoI; supplier: Pathogen-challenge series. Tubers
from pathogen-free Solanum tubercoum var. Shepody, clone
1756, were inoculated with 5 ul of Phytophthora infestans
(A2-mating type), through 2 puncture wounds 3 cm apart.
The tubers were incubated 1 minute to allow inoculum
absorption. The infection area was outlined for future
collection reference. Surface slices were sampled from the
tubers at 1 day, 5 days, 7 days, 11 days and 14 days
post-infection. All samples were pooled and used for RNA
isolation and library construction. A normalized library
was constructed following a modified protocol of Bonaldo
et al. (1996. Genome Research 6: 791-806)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CysPro---GluValGlnAlaLeuAsn---ArgAsnLeuValGlyPheGlyGluHisThr 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspProGlnIleIleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIleCysLeu
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1168
227
33
3
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
Gaps:
                      /tissue_type="Tubers"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x DN589159 (1-893)
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868.50
79.92%
68.85%
49.69%
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Best Local Similarity:
Query Match:
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/ctous_infercar.class
/notes="Vector: pBlusescript II SK+; Site I: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
for 1 days prior to harvesting a primer consisting of a
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into blub host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
                    Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

When it has been determined, an EST from the other end of this

clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD

877006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)

High quality sequence stop: 426.
                                                                                                                                                                                                                                           1. .566
/organism="Glycine max"
/organism="Glycine max"
/orltivar="Williams"
/db_xrefe"taxon:3847"
/dclone="SOYBEAN CLONE ID: Gm-c1066-4957"
/tibsue type="Leaf and shoot tip, salt stressed, 2 week old seedling"
/lab host="DH108"
/clone_lib="Gm-c1066"
/clone_lib="Gm-c1066"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 ATAGTGAAGGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCATTA
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  Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, R., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST project
Unpublished (1999)
                                                                                                                                               LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
                                                                                                                                                                              512
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93 ATCGTTAATGCCTGCGAAGAATTCGGATTCTTCAAAATCATAAACCATGACGTTCCTATG 152
                                                                                                 212
                                                                                                                                                                                                                                                   GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120
                                                                                                                                                                                                                                                                             LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 AATTCTTCTTCGTCAATGTTGGTGACTCATTGCAGGTTATGACTAACGGAAGGGTTAAG 752
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                                                GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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Public Soybean EST Project
Washington University School of Medicine
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694 bp mRNA linear EST 11-JUL-2001
mRNA sequence.
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Lycopersicon esculentum
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 694)
van der Hoeven, R., Sun, H., Bezzerides, J., Cho, J., Utterback, R.,
Ronning, C. and Tanksley, S.
Ronning, C. and Tanksley, S.
Generation of ESTs from Tomato Suspension Cultures
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 IleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 ATAACGCATAGGAATGTGTTGAGTATGTTGCTGAACGATGAGAAGAGGAGTGATTCTTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 ArgLeuAsnHisTyrProProCysProGlu 190
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84.74%
83.16%
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Other ESTS: BU544870 corresponding to Gm-r1088-979 (3')

Other ESTS: BU544870 corresponding to Gm-r1088-979 (3')

Contact: Shoemaker R/Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810
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/note="Vector: pSPORTI; Site_1: SalI; Site_2: NotI; This cDNA library was constructed_from mRNA isolated from seed coats (100-200mgs) of greenhouse grown plants. The library was prepared using the Life Technologies pSuperScript CDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The CDNA fragments were directionally cloned into the Not I sal I restriction site of the pSPORTI vector. The ligated cDNA fragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1472 Std Error: 0.00
High quality sequence stop: 436.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               AW184969 EST 24-JUL-2004 653 bp mRNA linear EST 24-JUL-2004 se84f09.yl Gm-c1023 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1023-1410 5' similar to TR:O04162 O04162 DIOXYGENASE. ;, mRNA
                                                                                                                                 497
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378 AAGTCACAGTTCATTTTCCGAGAAAGTCCTCAGAATTTCAGGGTGGTCGTTGAGGAGTAC 437
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/clone="GRNOME SYSTEMS CLONE ID: Gm-c1023-1410"
/tissue type="seed coats of greenhouse grown plants"
/lab_host="DH10B"
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/cultivar="T157"
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140 GlyAspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerPro 120 141 IleThralaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGly 160 100 383 443 503 563 84 ATGGTTGTTCTTCTCTCAGCCAGCATTAAACCAGTTTTTCCTTCTGAAAACATGCAAGCCC 143 144 ACGCCCTIGTTCGCGGGGATTCCTGTGGTCGACCTCACGGACCCCGATGCCAAGACCCAC 203 204 ATAGTCAATGCCTGCAGGGACTTCGGCTTCTTCAAGCTCGTGAACCACGGTGTTCCGTTA 263 8 40 9 transformed into E.coli Electromax DH10B host cells. Th library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna." MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu ... LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArglleGlyProAsn 324 AAAGACAGGCTGGTCCCCCTGACCCTTTTGGCTACGGCAGCAAGAGGATTGGCCCTAAC 384 GGGATGTCGGTTGGGTCGAATACCTCCTTCTCAACACCCAACCCTGATGTCATCTCCCCC LysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 504 ATTAGAGCGGTGAAGAACATGTGCTATGAGGTGTTGGAATTGATGGCTGANGGATTGTGG Thr ProLeu Phe Thr Glylle ProVal Val Aspleu Thr His ProAspAla Lys Asn Leu IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu 653 3 3 29 0 0 Length: Matches: Conservative: Mismatches: Indels: (1-653)x AW184969 09e-86

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EST 27-APR-2005
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1 (bases 1 to 755)
1 (bases 1 to 755)
Strugane, T., Watanabe, M., Yano, K., Suzuki, H., Sakurai, N. and Shibata, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 ATCGTTAATGCCTGCGAAGAATTCGGATTCTTCAAAATCATAAACCATGACGTTCCTATG 157
                                                                                                                                                                                                                                           BW690134 Incopersicon esculentum cv. Micro-Tom fruit Lycopersicon esculentum cv. Micro-Tom fruit Lycopersicon esculentum cDNA clone FC17CG04 5', mRNA sequence.
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/mol type="mkina"
/mol type="mkina"
/cultivar="mkina"
/db_xref="taxon:4081"
/clone="FC17C094"
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/clone="fruit"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetValValleuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tags of full-length cDNA clones prepared from the laboratory-grown miniature tomato (Lycopersicon esculentum) cultivar Micro-Tom Unpublished (2005)
Contact: Daisuke Shibata
        543 TCAAGACTATCAATGATATATTTTGGAGGACCACCATTGAGTGAAAGGATAGCACCATTG
                                            290 ProSerValMetLeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyr
                                                                                 603 ccarcacraarg---Gaagggaaagacagrrraracaaagagrrracarggrrrcagrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 ThrproLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kazusa DNA Research Institute;
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan Tel: 81-438-52-3947
Fax: 81-438-52-3948
Email: shibata@kazusa.or.jp.
Location/Qualifiers
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                                                                                                                                            660 CAAAAGTCAGCTTACAAGACTAGACTAGACTGAT 692
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XhoI; Suspension cultures of L.esculentum E6203 were grown
in Murashige and Skoog based medium, supplemented with 15%
autoclaving), 2% saccharose, and lmg/ml 2,4D (pH5.8).
Fresh medium was added every 7 days, and cultures were
grown at 25 C, with 12hrs of light and continuous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerArgLeuSerMet11eTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeu 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 LeuAsnThrAsnProAspVallleSerProLysSerLeuCysIlePheArgGluAsnPro 130
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|TTCAACAAATTCTGAATTCAATTACCAGAAATTCGCATCTGTATTAGGTGTCAATCCA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 HisHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242
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Contact: CUGI
Clemson University Genomics Institute
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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152
35
2
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Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases I to 776)
Tsugane, T., Watanabe, M., Yano, K., Suzuki, H., Sakurai, N. and Shibata, D.
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LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArgIleGlyProAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                            ThrserPhePheIleAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPhe 256
                                                                  ArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsn------
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-25-1947
Fax: 81-438-52-3948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Lycopersicon
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54.5 53.6 11 936.5 December 28, 2005, 01:23:14; Search time 249 Seconds (without alignments) 2362.943 Million cell updates/sec US-10-670-454-2 1748 1 MVVLSQPALNQFFLLKPFKS......AAYTSRLADNRLAPFQKSAA 331 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. - nucleic search, using frame\_plus\_p2n model Total number of hits satisfying chosen parameters: 1303057 segs, 888780828 residues BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Copyright Title: Perfect score: Sequence: Scoring table:

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Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*

/cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\* Issued

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 1, Appli	Sequence 62, Appl	Sequence 7, Appli	Sequence 13, Appl	Sequence 5, Appli	Sequence 64, Appl	Sequence 3, Appli	Sequence 7, Appli	Company 1
SUMMARIES	ID	US-09-719-108-1	US-09-371-307-62	US-09-719-108-7	3 US-09-614-912-13	US-09-614-912-5	US-09-371-307-64	US-09-614-912-3	US-09-614-912-7	1-610-614-01-011
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Best Local Similarity:
Query Match:
DB:
 Sequence 62, Applicat
Patent No. 6723897
GENERAL INFORMATION:
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                                 MetValValLeuSerGlnProAlaLeuAsnGl
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APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Logusch, Eugene W.
APPLICANT: Logusch, Bugene W.
APPLICANT: Logusch, Sherry J.
APPLICANT: Raw, Joah Sherry J.
TITE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOST: 216
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARR: Patentin Ver. 2.0
SOFTWARR: Patentin Ver. 2.0
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Matches:
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37 AlaLysAsnLeuIleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis
                                                    Glyval ProLeuGluLeuMet AlaAsnLeuGluAsnGluAlaLeuArgPheLysLys
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Patent No. 6677502
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Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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                                                                                                                                        TTTTCATCAATGTTGGTGACACTCTTCAGGTAATGACTAATGGGAGGTTTAAAAGTGTA
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                                                                                                                                                                               LysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGly
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                                         GGATTTGGAGGAGCACACAGACCCACAGATAATTTCTGTCTTGAGATCTAACAGCACCTCA
                                                                  GlyLeuGln11eCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer
                                                                                             762 GGCCTGCAAATCTGTCTCACAGATGGCACTTGGGTTTCTGTCCCACCTGATCAACTTCC
                                                                                                                        PhePheileAsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerVal
               GlyPheGlyGluHisThrAspProGlnIle11eSerValLeuArgSerAsnSerThrSer
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Mismatches:
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APPLICANT: Hodden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TITLE OF INVERTION: Gibberellin 2-Oxidase;
FILE REFERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: PCT/GB99/01857
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SQ ID NOS: 16
SGO ID NO 7
SEQ ID NO 7
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Matches:
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Patent No. 6670527
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; ORGANISM: Arabidopsis thaliana
US-09-719-108-7
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1092.50
76.81%
63.25%
62.50%
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Best Local Similarity:
Query Match:
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        747 TTTGGAGAACACACAGACCCACAAATCATCTCTCTGTTAAGATCCAACAACAACTTCAGGC
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                                                                                      PheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGly
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APPLICANT: Famodu, Omolayo O.
APPLICANT: Famodu, Omolayo O.
APPLICANT: Bee, Jian Ming
APPLICANT: Bakai, Hajime
APPLICANT: Wangi, Zude
APPLICANT: Gaimi, Perry G
APPLICANT: Anderson, Shawn
ITILE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PLLING DATE: 1999-12-15
PRIOR PLLING DATE: 1999-12-21
PRIOR PLLING DATE: 1999-12-21
PRIOR PLLING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SEQ ID NOS: 204
SEQ ID NOS: SEQ 
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Patent No. 6677502
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Orozco, Buddy
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CRGANISM: Glycine
US-09-614-912-5
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APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA.
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT APPLICATION NUMBER: 60/143,401
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: 60/172,946
PRIOR FILING DATE: 1999-12-21
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Matches:
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77.95%
60.73%
61.13%
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SOFTWARE: Microsoft C
SEQ ID NO 13
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Pred. No.:
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                                                                                              APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Filch, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Ream, Joel B.
APPLICANT: Ream, Joel B.
APPLICANT: Ream, Joel B.
APPLICANT: Ream, Joel B.
APPLICANT: Logusch, Sherry J.
TILE REPRENCE: MOBT:216
CURRENT APPLICANT: NUMBER: US/09/371,307A
CURRENT FILNG DATE: 1999-08-10
NUMBER CF SEQ ID NOS: 89
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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                                          US-09-371-307-64
; Sequence 64, Application US/09371307A
; Patent No. 6723897
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APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REPERENCE: BB1379 US NA
CURRENT PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 1999-07-12
PRIOR PILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR FILING DATE: 1999-07-2
PRIOR APPLICATION NUMBER: 60/145,50
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
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PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-12
PRIOR PILING DATE: 1999-12-21
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Patent No. 6677502
GENERAL INFORMATION:
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Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
Lee, Jian Ming
Sakai, Hajime
Weng, Zude
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SOFTWARE: Microsoft O
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 ACGGACACGATGGACAAGGCCGAGAGCCGTCAGGTTCTTCTCCCAGACGCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluLygAgpArgAlaGlyProProAgpProPheGlyTyrGlySerLygArg1leGlyPro
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       Length:
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 100 AsnGlyAspValGlyTrpValGluTyrLeuLeuLeuLeuAsnThrAsnProAspVallleSer 119
                                                                           120 ProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsn 139
                                                                                                     118 CTCTCCGGCGCTGCGCCGTC---CCGTCCTGCGCGCTCTTCCGGGCGCGCTGAACGAG 534
                                                                                                                                                                                                                               GlylleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAspSerCys 179
                                                                                                                                                                                                                                                                                                         PheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuVal 199
                                                                                                                                                                                                                                                                                                                               GlyLeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSer 239
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                                                                                                                                                                                                                                                       LysHisArgValLeuAlaAspThTThrLysSerArgLeuSerMetIleTyrPheGlyGly
                                                                                                                                                      TyrileThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeu
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APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Goot-Buddy
APPLICANT: Famodu, Cmolayo O.
APPLICANT: Famodu, Cmolayo O.
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Weng, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1379 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/143,412
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/146,650
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Patent No. 6677502
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194
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86
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Conservative:
Mismatches:
Indels:
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APPLICANT: Eamodu, Omolayo O.
APPLICANT: Eee, Jian Ming
APPLICANT: Sakai, Hajime
APPLICANT: Sakai, Hajime
APPLICANT: Gaimi, Perry G
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
FILE OF INVENTY ON PUBER: US/09/614,912
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PILING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-21
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Matches:
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                                                                                                            Sequence 7, Application US/09614912
Patent No. 6677502
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                                                                                                                                                                      Allen, Steve
Rafalski, Antoni
Orozco, Buddy
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; ORGANISM: Triticum aestivum
US-09-614-912-7
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LysAspArgAlaGlyProProAspProPheGlyTyrGlySerLysArg1leGlyProAsn 100
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        41 IleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHisGlyValProLeu
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                                                                                                            274 MetileTyrPheGlyGlyProAlaLeuSerGluAsnileAlaProLeuProSerValMet
                                                                                                                                                                                                                      934 TTCATCTACTTCGCGGGGCCGCCGCTGGGGCAGCGGATCGCGCCGCTGCCGCAGTGCTG
                                                                                                                                                                                                                                                                                                294 LeuLysGlyGluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAla
                                                                                       GlyArgPheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSer
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APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Phillips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT APPLICATION NUMBER: EQG 9812821.8
PRIOR PILING DATE: 1999-06-11
PRIOR PILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 1008
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US-09-719-108-9
; Sequence 9, Application US/09719108
; Patent No. 6670527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-719-108-9
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PRIOR APPLICATION NUMBER: 60/1/0,200
PRIOR FILING DATE: 1999-12-15
PRIOR PEPLICATION NUMBER: 60/172,959
PRIOR PELING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
FUNCTH: 1555
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957.50
70.75%
57.01%
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Best Local Similarity:
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ORGANISM: Zea mays
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Pred. No.:
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US-09-614-912-1
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                                                                                                                                                                                                                      ) ORGANISM: Arabidopsis thaliana

; FEATURE:

; NAME/KRY: misc feature

; LOCATION: (1243, 1265)

; OTHER INFORMATION: unidentified

US-09-719-108-5
                                                                                               1.14e-104
936.50
72.16%
55.39%
53.58%
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Best Local Similarity:
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                                                                          LysSerLeuCysllePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr
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APPLICANT: Hodden, Peter
APPLICANT: Hodden, Peter
TITLE ON THINIDED, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION NUMBER: US/09/719,108
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR APPLICATION NUMBER: GB 9815404.0
PRIOR APPLICATION NUMBER: GB 9815404.0
SOFTWARE: PATENT UN ONE: 16
SOFTWARE: PATENT UN OS: 16
SOFTWARE: PATENT UN OS: 16
SEQ ID NO 5
SEQ ID NO 5
TYPE: DNA
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Patent No. 6670527
GENERAL INFORMATION:
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Conservative: Mismatches: Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 AsnLeuGluAsnGluAlaLeuArgPhePheLysSerGlnSerGluLysAspArgAla 84
                                                                                                                                                                              264 LeualaAspThrThrLysSerArgLeuSerMetlleTyrPheGlyGlyBroalaLeuSer
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                                                                                                                                  GTTGGTGACTCCTTACAGGTAATGACCAATGGAAGGTTTAAAAGTGTAAAAACATAGGGTA
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                                                                                                                                                                                                                                               GluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeuTyrLysGlu
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                                                                                                                ValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArgVal
                                                224 CysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhePheIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09371307A

Sequence 58, Application US/09371307A

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Piller, Kenneth J.

APPLICANT: Elich, Tedd D.

APPLICANT: Loguench, Eugene W.

APPLICANT: Loguench, Eugene W.

APPLICANT: Ream, Joel E.

APPLICANT: Ream, Joel E.

APPLICANT: Ream, Joel E.

APPLICANT: Reprincible Sherry J.

FILE REFERENCE: MOBT:216

CURRENT PPLING DATE: 1999-08-10

NUMBER OF SEQ IN NOS: 2.0

SONTARE: Patentin Ver. 2.0
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; ORGANISM: Arabidopsis thaliana
US-09-371-307-58
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                                                                                  LeuLeuAsnThrAsnProAspVallleSerProLysSerLeuCysIlePheArgGluAsn 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 -----TTGAGGGTGGCTTTGAATAATTATATGAAATCAGTAAAGAAAATGGCGTGT 108
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   275 IleTyrPheGlyGlyProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
                    204 HisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSerGlyLeuGlnIle 223
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APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filter, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Rogusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOST: 1999-08-10
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT APPLICATION NUMBER: US/08-10
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 673
                                                                                                                                                   315 ThrSerArgLeuAlaAspAsnArgLeuAlaProPheGlnLys 328
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                                                                                                                                                                                                                        Sequence 67, Application US/09371307A Patent No. 6723897 GENERAL INFORMATION:
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LOCATION: (726)
OTHER INFORMATION:
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  AGAATGGAGCAAGAGTCTATAAACTTCTTTGCTAAACCGGGCTCACGAGAAGAAATCTGTC 222
                                                               GlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspValIleSerProLysSerLeu 123
                                                                                                                                                 ValLysAsnMetCysTyrAlaValLeuGluLeuMetAlaGluGlyLeuGlyIleArgGln 163
                                                                                                                                                                                                                                    HisTyrProProCysProGluVal-------GlnAlaLeuAsn 195
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                                  124 CysIlePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyrIleThrAla
                                                                                                                     CTGACAAGAGTTGGCTTCGGAGAACACCGACCCTCAGATTTTAACAGTTCTTAGATCT
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GGTGAGGTCGAGTATTTGCTGTTTCACTAACGACCCTGCC------
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Factor No. 6723897

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Holer, Greneth J.

APPLICANT: Filer, Tedd D.

APPLICANT: Elich, Tedd D.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Tedd D.

APPLICANT: Block, Tedd D.

APPLICANT: Block, Ganesh M.

APPLICANT: Block, Mayene W.

APPLICANT: Ream, Joel E.

APPLICANT: Ream, Joel E.

TITLE OF INVENTION: Methods for controlling gibberellin levels

FILE REBERBENGE: NOBT:216

CURRENT APPLICATION NUMBER: US/09/371,307A

CURRENT FILING DATE: 1999-08-10
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APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Tedd D.
APPLICANT: Elich, Tedd D.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFERENCE: MOBT:216
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Patent No. 6723897
GENERAL INFORMATION:
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31.64%
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 71
; LENGTH: 811
; TYPE: DNA
; ORGANISM: Zea mays
US-09-371-307-71
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Best Local Similarity:
Query Match:
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183 AsnHisTyrProProCysProGlu---ValGlnAlaLeuAsn------ArgAsnLeu 198
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CURRENT APPLICATION NUMBER: US/09/371,307A CURRENT FILING DATE: 1999-08-10 NUMBER OF SEQ ID NOS: 89 SSCTWARE: Patentin Ver. 2.0 SSCTARE: SEQ ID NO 68 LENGTH: 406
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                                                                   TYPE: DNA
ORGANISM: Gossypium hirsutum
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NAME/KEY: unsure

LOCATION: (306)

OTHER INFORMATION: n = US-09-371-307-68
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67, Appl 67, Appl 16086, Appl 16086, Appl 129307, 766, Appl 58, Appl 2, Appl 2, Appl 159585, 34429, A

71, Appl 71, Appl 20123, A 614, App 9278, Ap

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Title: Perfect score:

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Sequence:

Scoring table:

Searched:

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Sequence 3, Application US/10821711

| Sequence 3, Application No. US2004023142A1
| Publication No. US2004023142A1
| GENERAL INPORMATION:
| APPLICANT: Gilbertson, Larry A
| APPLICANT: Krieger, Elysia K
| APPLICANT: Talang, Wanggen
| APPLICANT: The Constructs and Methods To Enhance THE PRODUCTION OF
| TITLE OF INVENTION: DNA CONSTRUCTS AND METHODS TO ENHANCE THE PRODUCTION OF
| TITLE OF INVENTION: COMMERCIALLY VIABLE TRANSCENIC PLANTS
| FILE REFERENCE: 38-21 (52867) B
| CURRENT FILING DATE: 2004-04-08
| PRIOR FILING DATE: 2004-04-08
| PRIOR FILING DATE: 2003-04-09
| NUMBER OF SEQ ID NOS: 16
| SEQ ID NO 3
| LENGTH: 999
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; ORGANISM: Phaseolus
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-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cqn2 1/USPTO_epool/US10670454/runat_27122005_124842_29154/app_query.fasta_1.519
-Q=/Cqn2 1/USPTO_epool/US10670454/runat_27122005_124842_29154/app_query.fasta_1.519
-Q=/Cqn2 1/USPTO_epool/US10670454 or -UNITS=bits -SUPFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.odi -LIST=45 -DOCALIGN=200 -TRR_SCORE=pct
-HRAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LCCAL_OUTFFWT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LCCAL_OUTFFWT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LCCAL_OUTFFWT=pto -NORM=ext
-NSR=uS10670454 occan 1 1 1026 or unat 27122005 124842 29154 -NCFU=6 -ICFU=3
-NORM=PCT=120 -WARN TIMEOUT=30 -FRABS=1 -XGAPPO=10 -KGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 62, Appl
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Sequence 62, Appl
Sequence 1350, Ap
Sequence 7, Appli
                                                                                                             December 28, 2005, 01:30:23 ; Search time 975 Seconds (without alignments) 2807.348 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/USO7 FUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/USO9 FUBCOMB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO9A FUBCOMB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO9B FUBCOMB.seq:*
5: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
6: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
7: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
8: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
9: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
10: /cgn2 6/ptodata/1/pubpna/US1OB FUBCOMB.seq:*
                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                OM protein - nucleic search, using frame_plus_p2n model
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US-10-670-454-1
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US-10-670-454-7
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Best Local Similarity:
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                                                                                                                                 GluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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                  MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer
                            ABRARGLeuAlaProPheGlnLysSerAlaAla 331
US-10-670-454-2 (1-331) x US-10-821-711-3 (1-999)
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GENERAL INFORMATION:
APPLICANT: Thomas, Stephen G
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hilips, Andrew L
TITLE OF INVENTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.097000
CURRENT APPLICATION NUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR PILING DATE: 2003-09-26
PRIOR PILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: PCT/GB99/01857
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-07-15
SEQ ID NOS: 16
SOFTWARE: PATENTIN VET: 2.1 Indels: 3.55e-219 1748.00 100.00% 100.00% coccinens TYPE: DNA ORGANISM: Phaseolus 181

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Sequence 1, Application US/10670454

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                                                  GlubeuMetAlaAsnLeuGluAsnGluAlabeuArgPhePheLysLysSerGlnSerGlu
                                                               GlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsnSerThrSer
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; Publication No. US20030233679A1
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Filler, Kenneth J.
; APPLICANT: Filch, Tedd D.
; APPLICANT: Blich, Tedd D.
; APPLICANT: Rao, Sudabathula
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US-10-401-321-62
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LeuGlnIleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhe
                                                                                                                    Sequence 62, Application US/09371307A

Sequence 62, Application US/09371307A

Patent No. US20020053095A1

GENERAL INFORMATION:

APPLICANT: Brown, Sherri M.

APPLICANT: Filey, Kenneth J.

APPLICANT: Elich, Tedd D.

APPLICANT: Loguench, Eugene W.

APPLICANT: Loguench, Eugene W.

APPLICANT: Ram, Joal E.

APPLICANT: Ream, Joal E.

APPLICANT: Loguench, Sherry J.

TITLE OF INVENTION: Methods for controlling gibberellin levels

FILE REFERENCE: MOBT: 216

CURRENT APPLICANTON NUMBER: US/09/371,307A

CURRENT APPLICANT: 1999-08-10

NUMBER OF SEQ IN NOS: 2.0
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Matches:
Conservative:
Mismatches:
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90.36%
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CORGANISM: Glycine max
US-09-371-307-62
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Best Local Similarity:
Query Match:
DB:
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US-09-371-307-62
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Sequence 1350, Application US/09938842A

Sequence 1350, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT PILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR PELING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1350

LENGTH: 1026
                                                                                                                                  ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCys 299
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APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
APPLICANT: Logusch, Sherry J.
APPLICANT: Baerson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216--1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
LENGTH: 1359
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
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                     ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1350
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SEQ ID NO 1350
LENGTH: 1026
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US-09-938-842A-1350
; Sequence 1350, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Joef
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLAN; TITLE OF INVENTION: SAME, AND METHODS OF USE; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLAN; TITLE OF INVENTION: SAME, AND METHODS OF USE; TITLE OF INVENTION: SAME, AND METHODS OF USE; TITLE OF INVENTION WINBER: US/09/938,842A
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR APPLICATION NUMBER: US/09/938,842A
; PRIOR APPLICATION NUMBER: US/09/938,842A
; PRIOR PILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                      177 AspSerCysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArg 196
                                                                                                                                                                                                                           197 AsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerValLeuArgSerAsn
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                                                                                                                                                         GTGAAGGTGGGGTTTTGGGGAACACACAGACCCACAGATAATCTCAGTGCTAAGATCTAAT
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                                                                   ValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMetAla
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Filer, Kenneth J.
APPLICANT: Elich, Tedd D.
APPLICANT: Loguesch, Eugene W.
APPLICANT: Ream, Joel B.
APPLICANT: APPLICANT: MOBT: 216
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOUTHARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 1403
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Matches:
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1060.00
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) ORGANISM: Glycine max
US-09-371-307-64
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Pred. No.:
Score:
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US-09-371-307-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaLysAsnLeulleValAsnAlaCysArgAspPheGlyPhePheLysLeuValAsnHis
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                                                  GluGluCysLeuTyrLysGluPheThrTrpCysGluTyrLysLysAlaAlaTyrThrSer
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                           Sequence 7. Application US/10670454
Fublication No. US20040229357A1
GENERAL INFORMATTON:
APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
TITLE REPERENCE: 0623.097000
CURRENT PHILIPS, Andrew L
TITLE REFERENCE: 0623.097000
CURRENT FILING DATE: 2003-09-26
FRIOR APPLICATION NUMBER: US/10/670,454
CURRENT FILING DATE: 2000-12-08
FRIOR APPLICATION NUMBER: ECT/GB99/01857
FRIOR FILING DATE: 1999-06-11
FRIOR FILING DATE: 1999-06-11
FRIOR FILING DATE: 1999-06-12
FRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 16
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; ORGANISM: Arabidopsis thaliana
US-10-670-454-7
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1092.50
76.81%
63.25%
62.50%
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Best Local Similarity:
Query Match:
DB:
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                                                                                         APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Filler, Kenneth J.
APPLICANT: Kilahore, Ganesh M.
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Sudabathula
APPLICANT: Rao, Joale W.
APPLICANT: Barson, Scott R.
TITLE OF INVENTION: Methods for Controlling Gibberellin Levels
FILE REFERENCE: 11899.0216.DVUS01 (MOBT:216-1)
CURRENT APPLICATION NUMBER: US/10/401,321
CURRENT APPLICATION NUMBER: US/10/401,321
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Mismatches:
Indels:
    1091 AATAGGCTTGGACATTTTGAGAGAATTGTTGCT 1123
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Matches:
                                                       ; Sequence 64, Application US/10401321; Publication No. US20030233679A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     2.06e-128
1060.00
76.44%
60.42%
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; ORGANISM: Glycine max
US-10-401-321-64
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Best Local Similarity:
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US-10-401-321-64
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raCaAaGaGTTTACGTGGTTCGAGTATAAAAATTTAACCTATGCTTCAAGATTGGCTGGT 1090
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                                                                                                 MetValValLeuSerGlnProAlaLeuAsnGlnPhePheLeuLeuLysProPheLysSer 20
                                                                                                                                                                                                             449 GGGGATGTTGGTTGGGTTGAGTACCTTCTTCTCAACAACAAGAA------
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                                                                                                                  ThrProLeuPheThrGlyIleProValValAspLeuThrHisProAspAlaLysAsnLeu
                                                                                                                                                                        GlubeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSerGlu
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APPLICANT: Kayano, Toshiaki
APPLICANT: Matsuoka, Makoto
APPLICANT: Kobayashi, Masatomo
APPLICANT: Saito, Tamio
APPLICANT: Sakamoto, Tomoaki
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: AR ROWALT Thomas J
APPLICANT: Avou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 21951
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ORGANISM: Oryza sativa
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APPLICANT: Sakai, Miho
TITLE OF INVENTON: GIBBERELLIN 2-OXIDASE GEN
FILE REFERENCE: SHZ-014
CURRENT APPLICATION NUMBER: US/10/392,325
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEG ID NOS: 7
PRIOR APPLICATION NUMBER: US/2002-276051
PRIOR FILING DATE: 2002-09-20
SOFTWARE: Patentin version 3.1
SEG ID NO 3
LENGTH: 984
                                                                                                                                                                                                      Length:
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72.67%
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                                                                                                             TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                       NAME/KEY: CDS
LOCATION: (1)..(984)
OTHER INFORMATION:
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Best Local Similarity:
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Pred. No.:
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Sequence 78659, Application US/10437963
; Sequence 78659, Application US/10437963
; Publication No. US20040123343A1
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Application Name
; APPLICANT: Cao, Yongwei
; APPLICANT: Bucharov, Andrey A.
; TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 30-21(53221)B
; CURRENT PRILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 78659
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PheLysSerValLysHisArgValLeuAlaAspThrThrLysSerArgLeuSerMetIle
                                                  760 TTCAAGAGCGTGAAGCACAGGGTGGTGGCCAACAGCCTAAAGTCTAGGGTTTCCTTCATC
                                                                                                                                 200 CCCGGCGACGTCTTCTCCGGCGTGCCGGTCGTCGACCTCGGCAGCCCCGGCGGGGGAGG
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US-10-437-963-78659
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|TCCAACGGCACTCCGGCCTGCAGATCGCGCTCCGCGACGGCGCGCAGTGGGTCCCGTG
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Matches:
Conservative:
Mismatches:
Indels:
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                                 Clone ID: MRT4577_163444C.1
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957.50
70.75%
57.01%
54.78%
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: C:
US-10-425-115-69575
                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: ANOWATION: Plants
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 69575
LENGTH: 1611
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 60 LeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSerGlnSer
            136 ValValGluAsnTyrIleThrAlaValLysAsnMetCysTyrAlaValLeuGluLeuMet ::: |||| ||| ||| |||
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                                                                                               116 AspValIleSerProLysSerLeuCysIlePheArgGluAsnProHisHisPheArgAla
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     LysSerLeuCys1lePheArgGluAsnProHisHisPheArgAlaValValGluAsnTyr 140
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                                    361 AAAACCACCGCCATTTTCCGGCACACCCCTGCAATTTTCAGAGAGGCAGTGGAAGAGTAC
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APPLICANT: Provart, Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Rick, Darrell
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
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CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR AFLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
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; Publication No. US20040010815A1
; GENERAL INFORMATION:
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Goff, Stephen A.
Katagiri, Fumiyaki
Kreps, Joel
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Briggs, Steven P.
Cooper, Bret
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Conservative:
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                                                                                                                                                                                                                                                                          APPLICANT: Thomas, Stephen G
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
APPLICANT: Hedden, Peter
TIED OF INVESTION: Gibberellin 2-Oxidase
FILE REFERENCE: 0623.0970000
CURRENT APPLICATION WUMBER: US/09/719,108
PRIOR APPLICATION NUMBER: US/09/719,108
PRIOR PILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR APPLICATION NUMBER: GB 9812821.8
PRIOR APPLICATION NUMBER: GB 9815404.0
                                                                                                                                                                                                                            ; Sequence 9, Application US/10670454; Publication No. US20040229357A1; GENERAL INFORMATION:
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; ORGANISM: Arabidopsis thaliana
US-10-670-454-9
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SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Oryza sativa
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APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960296.97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT APPLICATION NUMBER: US/10/155,435
PRIOR APPLICATION NUMBER: US/10/155,435
PRIOR PILING DATE: 2002-05-23
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
SSQ ID NO S
LENGTH: 1017
7 US-11-055-309A-2

7 US-11-034-771-1

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6 US-10-995-561-13513

6 US-10-995-561-13467

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7 US-11-021-086-43

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Sequence 3, Appli
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Sequence 3, Appli
Sequence 82, Appli
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Sequence 14, Appl
                                                                                                                                                         December 28, 2005, 01:42:45; Search time 786 Seconds (without alignments) 220.763 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd
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                                                     304 TTTGACAAGAAAAGTCGGAGAATTTTCCGCCGG-----AGTTACCGGG 354
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                                                                                                                                                                                                                               128 GluAsnProHisHisPheArgAlaValValGluAsnTyrIleThrAlaValLysAsnMet 147
                                                                                                                                                                                                                                                                                                                  460 ------ACBATGGAGABATTTGCTTCGGAATCAGAGCATTA 495
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                                         58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePhe-----
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                                                                                                                                                                                                                                                                               415 ATGACAGATATTTCTGACAACAAGACTTTACTACTCTCAGCTCA-----
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Sequence 3, Application US/11152892 Publication No. US20050251883A1 GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 TTTTCTGTGAAAGTCAGAGAAACGTTTTTCGGAC---TTATCGAAGAATAGTTACCGTTGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPheLysLysSer 77
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79
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110
66
APPLICANT: Amasino, Richard M.
APPLICANT: Schomburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Bizzell, Colleen M.
TITLE OF INVENTION: Dwarfism Genes and Dwarf Plants
FILE REFERENCE: 960.29-97605
CURRENT FILING DATE: 2005-06-15
PRIOR APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
PRIOR FILING DATE: 2005-06-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
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Matches:
Conservative:
Mismatches:
Indels:
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288.00
43.95%
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; LOCATION: (1)..(1008)
US-11-152-892-3
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Best Local Similarity:
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LENGTH: 1011
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3576 AATGICTITAAATTACTAGATTGTACTTATATATGTGTTTGGTTAGGCATGGAGCAATGG 3635
3279 TIGIATCAAGATCAAGTCGGAGGACTCCAACTT---ATCAAAGACAATAGATGGATCGCT 3335
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                                                       3396 CTTITATIATGICATICIACCATTACCATTATATCATTATCCGGAGCTTACAAATTAGTT
                                   ValProProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGlnVal----
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Matches:
Conservative:
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Publication No. US2005021883A1

GENERAL INFORMATION:

APPLICANT: Amasino, Richard M.

APPLICANT: Amasino, Richard M.

APPLICANT: Bizzell, Colleen M.

TILLE OF INVENTION:

FILE OF INVENTION: DWarfism Genes and Dwarf Plai

FILE OF INVENTION: DWARFS: US/11/152,892

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION NUMBER: US/11/152,892

CURRENT APPLICATION NUMBER: US/11/152,892

PRIOR FILING DATE: 2005-06-15

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 1

LENGTH: 2171
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Query Match:
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3171 TGTGTGAGAATACATGTTATCTAAGGATGAACGATATCCACCTTGTCCCAAACCATCG 3230
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 CCTCATACCGATACAAGTTTTCTCACTATACTCTCTCAAGATCAAATCGGAGGGTTAGAA 702
                                                                                                                                                                              ValLeuAlaAspThrThrLysSerArgLeuSerMetIleTyrPheGlyGlyProAlaLeu 282
                                                                                                                                                                                                                                                     SerGluAsnIleAlaProLeuProSerValMetLeuLysGlyGluGluCysLeu---- 300
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                                                       ::: :::||| |||:::||||| ||| TIG---GAAAATAATGGACCCTTACAGTC
                                     223 IleCysLeuThrAspGlyThrTrpValSerValProProAspGlnThrSerPhePhelle
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|GGATTTCTCCAGCAAATATCGAGAGGATGTCAATAGCTTTCTTCGTATGTCCTTATCTC
                                                                                                        AsnValGlyAspAlaLeuGlnValMetThrAsnGlyArgPheLysSerValLysHisArg
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61
107
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Publication No. US20050251883A1

GENERAL INFORMATION:
APPLICANT: Amasino, Richard M.
APPLICANT: Achouburg, Fritz M.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, Scott D.
APPLICANT: Michaels, US/11/152,892
CURRENT FILING DATE: 2005-06-15
FRICE REFERENCE: 960296,97605
CURRENT APPLICATION NUMBER: US/11/152,892
CURRENT FILING DATE: 2005-06-15
FRIOR APPLICATION NUMBER: US/10/155,435
FRIOR PILING DATE: 2002-06-23
NUMBER OF SEG ID NOS: 12

SOFTWARE PATENTIN VET. 2.1
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Matches:
Conservative:
Mismatches:
Indels:
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173.00
36.12%
20.91%
9.90%
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ORGANISM: Arabidopsis
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-11-152-892-2
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102 AspValGlyTrpValGluTyrLeuLeuLeuAsnThrAsnProAspVal---IleSerPro 120
                230 TrpValSerValProProAspGlnThrSerPhePheIleAsnValGlyAspAlaLeuGln 249
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1288 GTAATTACTTCTACCCTTTGATTTTCAACGTTCAAGTCCATTAAG 1332
                                                                              250 ValMetThrAsn-----GlyArgPheLysSerValLys 260
                                                                                                                                                                   US-LI-USB-81/A-3/C

Sequence 3, Application US/11058817A

Publication No. US20050262580A1

GENERAL INFORMATION:

APPLICANT: Petrukhin, Konstatin

APPLICANT: Petrukhin, Konstatin

APPLICANT: Petrukhin, Transgenic Mouse with a targeted

TITLE OF INVENTION: deletion of ELOVIA Gene

FILE REFERENCE: 21550

CURRENT APPLICATION NUMBER: US/11/058,817A

CURRENT FILING DATE: 2005-02-16

PRIOR FILING DATE: 2004-02-18

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH 967
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925 TTTTTCTGCTTTTTCCATTTTCTATCATGAGTTGTTTTTCT-
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Indels:
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Matches:
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Best Local Similarity:
Query Match:
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; ORGANISM: human
US-11-058-817A-3
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                                                                                                                   298 TTTTCTGTGAAAGTCAGAGAACGTTTTTCGGACTTATCGAAGAATAGTTACCGTTGGGGA 357
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118 CTTCCTGTGATCGATCTCAGCCATCTAACTAGTGGTGAGGAGGTCAAACGCAAAAGATGT 177
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                                                                                             ValProLeuGluLeuMetAlaAsnLeuGluAsnGluAlaLeuArgPhePheLysLysSer 77
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                                                   -----LeuLeuLeuAsnThrAsnProAspVallleSerProLysSer-----
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                                                                                                                                                                                  gLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeuValGlyPh 201
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                                                        68190 CTACTGCAACACTTCTTATCTATTTCTATTTTCAACTCTTGCCTTCCTCT-----
                                  -----LysAsnMetCysTyr-AlaValLeuGluLeuMetAlaGluGlyLeuGlyIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ROSENTELD, DEVLE
APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PLILING DATE: 2003-12-31
PRIOR FILING DATE: 2003-12-31
NUMBER OF SEC ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
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Conservative:
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Publication No. US20050260603A1
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GENERAL INFORMATION:
APPLICANT: MMI GENONICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
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Best Local Similarity:
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US-10-750-185-50357/c
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LENGTH: 1243
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GlyLeuGlyIleArgGlnArgAsnThrLeuSerArgLeuLeuLysAspGluLysSerAsp 177
                                                                         SerCysPheArgLeuAsnHisTyrProProCysProGlu--------ValGln 192
                                                                                                                                                 193 AlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIleSerVal 212
                                                                                                                                                                                    481 ATGAAGGAAAGAAACTTGGTTGTTTTTCTTTCTCAGAATAAAAAACACTGTGTCCAAATA 422
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Publication No. US20050266459A1
Publication No. US20050266459A1
Publication No. US20050266459A1
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT PILING DATE: 2005-05-04
PRIOR FILING DATE: 2005-05-04
PRIOR FILING DATE: 2004-05-04
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193 CAGCCACACAAACAGGAGATAAAAGAGTGCTTATAC 159
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                                  574 GGAATTCAACTGGGCTCCAAAAAATGCTTGTCC
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SOFTWARE: Patentin version 3.3
SEQ ID NO 82
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Qy 130 ProHisHisPheArgAlaValValGluAsn		TYPE: DNA   1
Qy         191 ValGlnAlaLeuAsnArgAsnLeuValGlyPheGlyGluHisThrAspProGlnIleIle         210           Db         824 GTTCAGGCT	Oy 266 AspThrThrLysSerArgleuSerMetlleTyrPheGlyGlyProhlaLeuSerGluhan 285	Alignment Scores:

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Sequence 27, Application US/11121086
FUBLication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
TITLE OF INVENTION: NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT APPLICATION NUMBER: 60/567,570
PRIOR PILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27
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Matches:
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Mismatches:
Indels:
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APPLICANT: Acresens, Jercen

APPLICANT: Acresens, Carlos

APPLICANT: Brain, Carlos

APPLICANT: Brain, Carlos

APPLICANT: Brain, Sadley

APPLICANT: Dain, Bradley

APPLICANT: Denton, R. Rex

APPLICANT: Judson, Richard S.

APPLICANT: Judson, Richard S.

APPLICANT: Aced, Carol R.

TITLE OF INVENTION: APOE Genetic Markers Associated with Age of Onset of Alzheimer's

TITLE OF INVENTION: Disease

FILE REFERENCE: 2300.0130001

CURRENT APPLICANTION NUMBER: US 60/538,590

PRIOR FILING DATE: 2004-01-22

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 1.
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4324 CITGGCGCACCTCCGCCACCTGCTCCTTCACCTCGAGGCGGTCGCGGGTCCGGCT 4265
                                                                                                                                                                                                                                                                                                          4488 TCGCTGGGCACAGGGGGGGGGCGCTGGTG---CCCACGGCAGCCTGCACCTTCTCCACCAGC 4432
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110 LeuLeuAsnThrAsnProAspValIleSerProLysSerLeuCysIlePheArgGluAsn 129
                                                                    130 ProHisHisPheArgAlaValValGluAsn-----
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NAME: WAGATKRY: misc feature
LOCATKON: (1102). (1102)
OTHER INFORMATION: n is 't'
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i_CCATION: (4553) ..(4533)
CTHER INFORMATION: n is 'c'
US-11-034-711-1
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NAME/KEY: misc feature
LOCATION: (1641)..(1641)
FEATURE:
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LOCATION: (4415)..(4415)
OTHER INFORMATION: n is 't'
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LOCATION: (2476)..(2476)
OTHER INFORMATION: n is 'g'
PEATURE:
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TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 8, Application US/10501675

Publication No. US20050282161A1

GENERAL INFORMATION:

HAPPLICANT: TARABE SEITYAKU CO., LTD.

TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.

CURRENT APPLICATION NUMBER: US/10/501,675

CURRENT APPLICATION NUMBER: US/2002-008435

PRIOR PILING DATE: 2002-01-17

PRIOR FILING DATE: 2002-01-17

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 3587
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ORGANISM: Homo sapiens
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; LOCATION: (99)
US-10-501-675-8
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US-10-501-675-8
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; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-)
US-10-995-561-13513
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| CGGCCCACTGGGGCTGCATGTCTTCCACCAGGGGCTCGAACCAGCTCTTGAGGCGGGCC 72624
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Sequence 13513, Application US/10995561

Sequence 13513, Application US/10995561

PUBLICATION NO. USCOOS272054A1

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DEPERTION AND USES THEREOF

TITLE OF INVENTION: DEPERTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                              GlyProAsnGlyAspValGlyTrp-------ValGluTyrLeu 109
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Matches:
Conservative:
Mismatches:
Indels:
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                                  US-10-670-454-2 (1-331) x US-11-121-086-27 (1-153142)
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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LENGTH: 40000
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ROSENFELD, David
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                                                                          1199 GGCCCACCTGTACGGGACCCTGAGTGGTCGCAGAGGGACCTGGAGGGACCTATCAGATA 1258
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                                                                                                rLeu------LeuLeuAsnThrAsnProAspVallleSerProLysSerLeuCysIl 125
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           AlaGlyProPro-AspProPheGlyTyrGlySerLysArgIleGlyProAsn----
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Sequence 34363, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
APPLICATY: WHI GENOMICS, INC.
APPLICATY: DeNISE, Sue K.
APPLICANT: KERR, Richard
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APPLICANT: BATES, Stephen
APPLICANT: BATES, Stephen
APPLICANT: FAMTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
TITLE OF INVENTION: COMPOSITION OF STEPHENCE: MMILLOO-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR PILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 34363
LENGTH: 1535
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Sublication No. US20050272054A1
GENERAL INFORMATION:
APPLICAMY: CARGILL, Michale et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOOUSES
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER: OF SEQ ID NOS: 85702
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13294
LENGTH: 15804
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652 GGAGGAGACGTCAGGCCGGCAACTCTGCGTAAGGTTTTGCCCTGTAGCACCGTC---- 599
                                                                                                 295 LysGlyGluGluCysLeuTyrLysGlu------PheThrTrpCys-----Glu 308
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                                          Gly------ProAlaLeuSerGluAsnIleAlaProLeuProSerValMetLeu 294
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OTHER INFORMATION: n = A,T,C or G,
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NAME/KEY: misc_feature
LOCATION: (1)...(15804
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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US-10-995-561-13294/c
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                                            179 CysPheArgLeuAsnHisTyrProProCysProGluValGlnAlaLeuAsnArgAsnLeu 198
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Job time : 891 secs
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